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**FIGURE 173**

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTTTGAAGGTCCTAGCCCACCTGGGCTGGCTC  
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCCGGACTCTGTCTGCTGCTTAAGGCCACTCC  
TATTCTACGGCTGACCCCTGGTGGTCACGTGGATCTGTTCCGCCACGCAAGTCTGGGTCCTTCG  
GCGATTGACCGGGGTCCTTGCTGTTCCGGGAGCCTCTCCTAAGCTGCCTGTTCCGCGGAGAGTT  
TGGAGGGGCGGGTTTGGGGTCGGTGTCTGATTGGGGCTCGCACCCGACGACGCTGGAGTCCCCG  
CTTAGGTACCAGTTAGCGTCAGGGGAGCTGGGTCAGGCGGTCGCCGGGACACCCCGTGTGTGG  
CAGGCGGCGAAGCGCTCTGGAGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC  
GGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGCCACGGCGGGCGGC  
CCTGGGAGCAGAGGTGGAGCGACCCCATACGCTAAAGATGAAGGCTGGGGTTGGCTGGCCC  
TGCTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG  
CATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCA  
TTCAGATGGGATCTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG  
CCCGCTCAGAGGCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG  
GGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAG  
AATCCAGTGAAGTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCTCAAGT  
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTCCCGAGAGG  
CTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACA  
TATCGCATGATGAGCTATGAACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGG  
AGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTAAAAAATA  
TGAAACCAAAAAGT

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**FIGURE 174**

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGS  
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGVRNGESSELDLQGIRID  
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCDHALHISHDEL

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 12-18, 16-22, 29-35

**Endoplasmic reticulum targeting sequence.**

amino acids 179-184



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**FIGURE 175**

CGCAGCGCGGCAGTCCTGATGCCCCGGCATGGGTACCGCTGCTGCCCCTGCTGTCGCTCCTG  
GTCGGCGCGTGGCTCAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAAGTGCAGGGTGGG  
AGATTCTGATGGGAACAAATTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGCG  
ACAGTGAAACCCTTTGCCATCGACATATTTCTGTACCAACAAAGATTTTCAGGGATTTTGTCT  
AGGGAGAAAAAGTATCGGACAGAAGCTGAGATGTTTGGATGGAGCTTTGTCTTTGAGGACTTT  
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA  
GTGGAAAAGGCATTTTGGAGGCAGCCTGCAGGTCCTGGCTCTGGCATCCGAGAGAGACTGGAG  
CACCCAGTGTTACACGTGAGCTGGAATGACGCGCGTGCCTACTGTGCTTGGCGGGGAAAACGA  
CTGCCCACGGAGGAAGAGTGGGAGTTTGCCGCCCCGAGGGGGCTTGAAGGGTCAAGTTTACCCA  
TGGGGGAACTGGTTCCAGCCAAACCGCACCAACCTGTGGCAGGGAAAGTTCCCCAAGGGAGAC  
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTTCCCCGCCAGAACAACACTAC  
GGGCTCTATGACCTCCTGGGGAACGTGTGGGAGTGGACAGCATACCGTACCAGGCTGCTGAG  
CAGGACATGCGCGTCTCCGGGGGGCATCCTGGATCGACACAGCTGATGGCTCTGCCAATCAC  
CGGGCCCCGGGTACCAACCAGGATGGGCAACACTCCAGATTCAGCCTCAGACAACCTCGGTTTC  
CGCTGTGCTGCAGACGCAGGCCGGCCGCCAGGGGAGCTGTAAGCAGCCGGGTGGTGACAAGGA  
GAAAAGCCTTCTAGGGTCACTGTCAATCCCTGGCCATGTTGCAAACAGCGCAATTCCAAGCTC  
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCCTTCCCTGTCTCCCATCCCTCTGTGGCAGGCGC  
CTCTCACCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTTGGAGAAGGGGGCCCAATGTGTGTT  
GACGATGGCTGGGGGCCAGGTGTTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAAA  
CACACAAACAGTTGGAACAGAGCACTCTGAAAGGCCATTTTTTAAGCATTTTAAAATCTATTC  
TCTCCCCCTTTCTCCCTGGATGATTCAGGAAGCTGACATTGTTTCTCAAGGCAGAATTTTCC  
TGGTTCTGTTTTCTCAGCCAGTTGCTGTGGAAGGAGAATGCTTTCTTTGTGGCCTCATCTGTG  
GTTTCGTGTCCCTCTGAAGGAACTAGTTTCCACTGTGTAACAGGCAGACATGTAAGTATTTA  
AAGCACAGTTCAGTCCTAAAAGGGTCTGGGAGAACCAGATGATGTACTAGGTGAAGCATTGCA  
TTGTGGGAATCACAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCCTATTCTTT  
TTTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCTTTCTCTGTTGCCAGGCTAGAGTGCCTG  
GTGATCACGGCTCACTCTAGCCTTGAATTCCTGGGCCCAAGCAATTCCTCCACCTCAGCCTCC  
TGAGTAGCTGGGACTACAAGTGTGCACCACCATGCCTGGCTAATTTTTTGAATTTTTGTAGTG  
ATGGGATCTCGCTCTGTTGCCAGGGTGGTCTCGAACTCCTGGCCTCAAGCGATCCTCCCACC  
TCGACCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCTCGCCTGGGCCCCCTTCTCCATA  
TGCCTCCAAAAACATGTCCCTGGAGAGTAGCCTGCTCCACACTGTCACTGGATGTCATGGGG  
CCAATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAA

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**FIGURE 176**

MARHGLPLLPLLSLLVGAWLKLGNQATSMVQLQGGRFLMGTNSPDSRDGEGPVREATVKPFA  
IDIFPVTNKDFRDFVREKKYRTEAEMFGWSFVFEDFVSDLRNKATQPMKSVLWWLPVEKAFW  
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ  
PNRTNLWQGKFPKGDKAEDGFHGVSPVNAFPAQNNGLYDLLGNVWEWTASPYQAAEQDMRVL  
RGASWIDTADGSANHRARVTTRMGNTPDASDNLGFRCAADAGRPPGEL

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 191-195

**N-myristoylation sites.**

amino acids 23-29, 25-31, 175-181

**Amidation site.**

amino acids 159-163

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**FIGURE 177**

GCCTTCTCGCGCCTGACCATGCACCCCTGCATCTTCCTGCTGGGCCACAGGCGAGCGCTTTAT  
TTCTGGAGCTGAGGGCTAAAACTTTTTTGAAGTTTCTTCTCCTCAACATCTGAATCATGCCAT  
GTGCCCAGAGGAGCTGGCTTGCAAACCTTTCCGTGGTGGCTCAGCTCCTTAACTTTGGGGCGC  
TTTGCTATGGGAGACAGCCTCAGCCAGGCCCGGTTGCTTCCCGGACAGGAGGCAAGAGCATT  
TTATCAAGGGCCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGGCATT  
TTTTGTCATATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTTGGATGGCT  
CAGAGGACTGGGTGTACTACAGAATTTCTCACGAGGAGAAGGACCTGTTTTTTAACTTGACGG  
TCAATCAAGGATTTCTTTCCAATAGCTACATCATGGAGAAGAGATATGGGAACCTCTCCCATG  
TTAAGATGATGGCTTCCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTTCTACAGCAGGGCA  
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTTTTCCAACCTACCAC  
ATGGAGACTTTTTTCAATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCCGC  
ACATCGTTTACAGGAGGCAGAAAGTTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA  
TTGTGACTCACATGTCCTCCTGGGTGAAGAATCTGTTTTGTTCTTTTGGTAGTTTTTATTAAA  
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTTTTTTAATATCTTCA  
TGACATTCAAATCTCTTCTGTATTCTCTTGCCAGAAAGTGATACATTCTTTTTTGCTTGATATAAA  
CCCTTTCACCTTGTC

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**FIGURE 178**

MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRFPDRRQEHFIKGLPEYHVVGPRVDAS  
GHFLSYGLHYPITSSRRKRDLGSEDWVYYRISHEEKDLFFNLTVNQGLSNSYIMEKRYGNL  
SHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHGLTGFFQLPHGDFFIEPVKKHPLVEGGY  
HPHIVYRRQKVPETKEPTCGLKGIVTHMSSWVEESVLFFW

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 11-15, 105-109, 125-129

**N-myristoylation site.**

amino acids 149-155

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**FIGURE 179**

CAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATACGAATTCCTTTTCT  
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGATATGTGTTGGATTACAGTTTTCTCT  
GCCTTGCCTACGACTGTTTCTGGTTGTTACCTGTTATCTTTTATTATTACTCCACAAAGAAAT  
ACTTGGATGTTCTGCTGTTTGTCTGAGCTCTGCACTGGGAGACAAATTAAGTCCGTAAGTCTAGG  
CCTTTGAGTATTCCCTAAGAATTTTCCTGAAAGTACAGTTTTTCTGTATCTGACTGGGAATAA  
TATATCTTATATAAATGAAAGTGAATTAACAGGACTTCATTCTCTTGTAGCATTGTATTTGGA  
TAATTCTAACATTCTGTATGTATATCCAAAAGCCTTTGTTCAATTGAGGCATCTATATTTTCT  
ATTTCTAAATAATAATTTTCATCAAACGCTTAGATCCTGGAATATTTAAGGGACTTTTAAATCT  
TCGTAATTTATATTTACAGTATAATCAGGTATCTTTTGTCCGAGAGGAGTATTTAATGATCT  
AGTTTCAGTTCAGTACTTAAATCTACAAAGGAATCGCCTCACTGTCCTGGGAGTGGTACCTT  
TGTTGGTATGGTTGCTCTTCGGATACTTGATTTATCAAACAATAACATTTTGAGGATATCAGA  
ATCAGGCTTTCAACATCTTGAAAACCTTGCTTGTTTGTATTTAGGAAGTAATAATTTAACAAA  
AGTACCATCAAATGCCTTTGAAGTACTTAAAGTCTTAGAAGACTTTCTTTGTCTCATAATCC  
TATTGAAGCAATACAGCCCTTTGCATTTAAAGGACTTGCCAATCTGGAATACCTCCTCCTGAA  
AAATTCAGAATTAGGAATGTTACTAGGGATGGGTTTAGTGGAATTAATAATCTTAAACATTT  
GATCTTAAGTCATAATGATTTAGAGAATTTAAATCTGACACATTCAGTTTGTAAAGAATTT  
AATTTACCTTAAGTTAGATAGAAACAGAATAATTAGCATTGATAATGATACATTTGAAAATAT  
GGGAGCATCTTTGAAGATCCTTAATCTGTCAATTTAATAATCTTACAGCCTTGCATCCAAGGGT  
CCTTAAGCCGTTGTCTTCATTGATTCATCTTCAGGCAAATCTAATCCTTGGAATGTAAGTCTG  
CAAATTTTGGGCCTTCGAGACTGGCTAGCATCTTCAGCCATTACTCTAAACATCTATTGTCA  
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAACATTACAAATTGTGTTACATC  
TTCAATAAATGTATCCAGAGCTTGCGCTGTTGTAAATCTCCTCATATTCATCACAAGACTAC  
TGCGCTAATGATGGCCTGGCATAAAGTAACCACAAATGGCAGTCCTCTGGAAAATACTGAGAC  
TGAGAACATTACTTTCTGGGAACGAATTCCTACTTCACCTGCTGGTAGATTTTTTCAAGAGAA  
TGCCTTTGGTAATCCATTAGAGACTACAGCAGTGTTACCTGTGCAAATACAACTTACTACTTC  
TGTTACCTTGAACCTGGAAAAAACAGTGCTCTACCGAATGATGCTGCTTCAATGTCAGGGAA  
AACATCTCTAATTTGTACACAAGAAGTTGAGAAGTTGAATGAGGCTTTTGACATTTTGCTAGC  
TTTTTTCATCTTAGCTTGTTGTTTTAATCATTTTTTTTGATCTACAAAGTTGTTTCAGTTTAAACA  
AAACTAAAGGCATCAGAAACTCAAGGGAAAATAGACTTGAATACTACAGCTTTTATCAGTC  
AGCAAGGTATAATGTAAGTGCCTCAATTTGTAACACTTCCCCAAATCTCTAGAAAGTCTGG  
CTTGGAGCAGATTGACTTCATAAACAAATTGTTCTGAAAATGAGGCACAGGTCATTCTTTT  
TGAACATTCTGCTTTATTAACTCAACTAAATATTGTCTATAAGAACTTCAGTGCCATGGACAT  
GATTTAACTGAAACCTCCTTATATAATTATATACTTTAGTTGGAAATATAATGAATTATATG  
AGGTTAGCATTATTAAATATGTTTTTTNTTAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 180**

MCGLQFSLPCLRLFLVVTCYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPESTV  
FLYLTGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPG  
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSQYLNLRNRLTVLGSGTFVGMVALRILDLSN  
NNILRISESGFQHLENLACLYLGSNNLTKVPSNAFEVLKSLRRLSLSHNP IEAIQPFAFKGLA  
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLKKNLIYKLDRNRIISI  
DNDTFENMGASLKILNLSFNNLTALHPRVLKPLSSLIHLQANSNPWECNCKLLGLRDWLASSA  
ITLNIYCQNPPSMRGRALRYINITNCVTSSINVSRAWAVVKSPHIHHKTTALMMAWHKVT TNG  
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTLNLEKNSALPN  
DAASMSGKTSLECTQEVEKLNEAFDILLAFFILACVLIIFLIYKVVQFKQKLKASENSRENRL  
EYYSFYQSARYNVTASICNTSPNSLES PGLEQIRLHKQIVPENEAQVILFEHSAL

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 530-547

**N-glycosylation sites.**amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,  
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

**N-myristoylation sites.**

amino acids 3-9, 69-75, 126-132, 174-180

**ATP/GTP-binding site motif A (P-loop).**

amino acids 506-514

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**FIGURE 181**

GGCCTGGCGCGGCGCTCCGGTAAGGCGTGTGTGCGGCAGGGCGGGGACAGAACCGTCTCTCG  
GGCTCTGGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG  
GCATTTCGTCCCCCTGGCACAGTTGGCCTCTTTCCAGAAGCCCGTTTTGTTTGTGTTTACGTCT  
AAATTCGCGTCGGTTCTTATTTCTCTCCCTGGCAAGGTCTGAAGACGGGTAGGAGAATAACCT  
GTGTCAGCGTGTTATGATGCCGTCCCGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGT  
GAAATATTCAAGGCTCTCCAGCACAGACGATGGCTACATTGACCTTCAGTTTAAGAAAACCCC  
TCCTAAGATCCCTTATAAGGCCATCGCACTTGCCACTGTGCTGTTTTTGATTGGCGCCTTTCT  
CATTATTATAGGCTCCCTCCTGCTGTGTCAGGCTACATCAGCAAAGGGGGGGCAGACCGGGCCGT  
TCCAGTGCTGATCATTGGCATTCTGGTGTTCCTACCCGGATTTTACCACCTGCGCATCGCTTA  
CTATGCATCCAAAGGCTACCGTGGTTACTCCTATGATGACATTCCAGACTTTGATGACTAGCA  
CCCACCCCATAGCTGAGGAGGAGTCACAGTGGAAGTGTCCCAGCTTTAAGATATCTAGCAGAA  
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTTGCAGATGTTTAAGAAAATAATGGCCAGATT  
TTTTGGGTCCTTCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT  
TTTCATCCCTGGGCCCTGACAAGTTTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA  
TTCTGTAATGGAAAAGTGTTGCCTGCCACCACCCTCTGTAGAGCTGAGCATTCTTTTAAATA  
GTCTTCATTGCCAATTTGTTCTTGTAGCAAATGGAACAATGTGGTATGGCTAATTTCTTATTA  
TTAAGTAGTTTATTTTAAAAATATCTGAGTATATTATCCTGTACACTTATCCCTACCTTCATG  
TTCCAGTGGAAGACCTTAGTAAAATCAAAGATCAGTGAGTTCATCTGTAATATTTTTTTTACT  
TGCTTTCTTACTGACAGCAACCAGGAATTTTTTTTATCCTGCAGAGCAAGTTTTCAAATGTAA  
ATACTTCCTCTGTTTAAACAGTCCTTGGACCATTCTGATCCAGTTCACCAGTAGGTTGGACAGC  
ATATAATTTGCATCATTTTGTCCCTTGTAATCAAGATGTTCTGCAGATTATTCCTTTAACGG  
CCGGACTTTTGGCTGTTTCCTAATGAAACATGTAGTGGTTATTATTTAGAGTTTATAGCCGTA  
TTGCTAGCACCTTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCCT  
AGAGGACTAGATCACCTTAGTTTGATTCTATTTTTTAGCTTGCAAAAAGTGACTTATATTCCA  
AAGAAATTTAAATGTTGAAATCCAAATCCTAGAAATAAAATGAGTTNNNTCCAAAAAAAAAA  
AAA

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**FIGURE 182**

MMPSRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLF~~LI~~GAFLIIIG  
SLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

**Transmembrane domains:**

amino acids 45-66, 79-95

**N-myristoylation sites.**

amino acids 11-17, 75-81



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**FIGURE 183**

CTAAAAAATACAAAAATTAGCTGGGCGTGGTGTGTCATGTACCTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGA  
GAATCGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATTAAGTCACTGCACTCCAGCCTGGGTGACAGA  
GCAAGACTCTGTATCAAAATAAATAAATAAAGTACAACCTCTGGATGGGCATGGTGGCTTATGTCTGTAATCCCAG  
CACTTTGGGAACCTTGAGGCGGGTAGATTGCTTGAGTCCGGGAGTTTGAGACCAGTCTGGGTAATATGGTAACCT  
GTCTACCAAAAAATACAGGTATTAGCCAGTCTCATAAAGTCTCGGTCTCAAAATAAATAAATAACATACATACATAGATG  
AAAATTTAAAAAATAAAGTCCAACCTCAGCGGTTTTCAGCATATTTACAGAGTTGTACAATCTTCACCACTATCTA  
ATTTTCAGAACATTTTCATCACCCCCAAAAGAAACCTAACCCATTGACTATCTCTCCATTTCTCCCTCTCCCTAG  
CCTCTGGCAACCACTAATCTCTTTTTTGTCTCTATAGATTTGCCTATTTTGGACAGTTTCATATACAAGGAATCAT  
ACCACATGTAGCCTTTTGTGTCCGGCTTCTTTGATTAATAGAATGTTTTCAAGGCTCATCTATGCTGTAGCCTGT  
ATCAGCACTTCATTCCTTTCTATGGCTGAATAATAGTCCACTGTAGGGATGTGCCATGTTTTTCCACTAGCTGAT  
GGACATTTGGGTTGTTTCCACCTTCTGGCTATTATAAATATTGCTGCTATAAATATTCACTTACAAGTTTTTGTG  
TGGACATATGTTTTTATTTCTTCTGGTATATCCTTCGGAGTGGAAGTCTGGATCAGGTGGTAAGTCTAGGTCTA  
ACCTGGCAGTTAAACAGAATCCTATGCATGCTGTAGTCCATGAGTTGAAATAAAGTCTGAGCCATAGTAAGTGC  
CAGATCATCTTCATTTACAGCAACCAAGTAATTTACAGATGAGGAAATGAAGGCTCCAGAGGTGAAGTGGCTT  
TTCCCATTTGAGCAGTTCCAAGTCAGACAGTTAAAAAGTGGCAGGACCTGGAAGAGAAGCTAGTTCTTTACCCCT  
GGCATTGAGGCTGCCTCCTGGGCTACGGGGCTGGCATTTAGAATAGAGCTAAGGCTGCTGCCAAGGCAGGTGC  
CCCAGTCTGCCCTCCTCTGTGCTCTTATTCACCTTTCTCTGCAGCCCTCCAGGGGACCCCTCTCTCAGCCACCCCTC  
TCTCTGGTGATGTCACAGTGCTGCCGGAAGATCAAAGATACGGTGCAGAACTGGCTTCGGACCATAAGGACATT  
CACAGCAGTGTATCCCGAGTGGGCAAAGCCATTGACAGGAACCTCGACTCTGAGATCTGTGGTGTGTGTGTCAGAT  
GCGGTGTGGGACGCGCGGAACAGCAGCAGCAGATCCTGCAGATGGCCATCGTGGAACACCTGTATCAGCAGGGC  
ATGCTCAGCGTGGCCGAGGAGCTGTGCCAGGAATCAACGCTGAATGTGGACTTGATTTCAAGCAGCCTTTCCCTA  
GAGTTGAATCGAATCCTGGAAGCCCTGCACGAACAAGACCTGGGTCTGCGTTGGAATGGGCCGTCTCCACAGG  
CAGCGCCTGCTGGAACCTCAACAGCTCCCTGGAGTTCAAGCTGCACCGACTGCACTTCATCCGCCTCTTGGCAGGA  
GGCCCCGCGAAGCAGCTGGAGGCCCTCAGCTATGCTCGGCACTTCCAGCCCTTTGCTCGGCTGCACCAGCGGGAG  
ATCCAGGTGATGATGGGCAGCCTGGTGTACCTGCGGCTGGGCTTGAGAGAAGTCACCCCTACTGCCACCTGCTGGAC  
AGCAGCCACTGGGCAGAGATCTGTGAGACCTTTACCCGGGACGCCTGTTCCCTGCTGGGGCTTTCTGTGGAGTCC  
CCCCCTAGCGTCAGCTTTGCCTCTGGCTGTGTGGCGCTGCCTGTGTTGATGAACATCAAGGCTGTGATTGAGCAG  
CGGCAGTGCAGTGGGGTCTGGAATCACAAGGACGAGTTACCGATTGAGATTGAACTAGGCATGAAGTGTGTTAC  
GCTCATCTGTGGCCATGTTATCTCCCGAGATGCACTCAATAAGCTCATTAAATGGAGGAAACACTCCGTGTTGCT  
TGCCCCATCCTCCGCCAGCAGAGCTCAGATTTCAACCCCTCCCATCAAGCTGAAGTGTCCCTACTGTCCCATGGAG  
CAGAACCCGGCAGATGGGAAACGCATCATATTCTGATTCCTACCTGGAAGGAATTTGTTGAAAGGGGTTTTTCAC  
CTGTGAGCCTTGGTCTGTCTCGGTAGGGTGGTCAACTTCAGTGGACTGTGGTTGGTTTCAGAGCGCCTGGCTGAG  
GAGTTCCACTGAGGGGAGCACTGGAGCAGCCCTTTGGCAGAGGCTGAGGAGGGAGATGGACCAGCCCACGCCTGG  
CACCTGGCTCCATGGCATAAGGAAAGGGAGATGCTGGCCTCTGTGCTCCTGCTGTCTTTTCTGTTTCTGTTTGC  
GTTTGACTTAGTAGCAACCGACAGAGTGGCAAGGGATTTGGTCTTCAGCAGTAGACATCCTTCCACCCCTGCCCT  
CAGCCAAGTCTCTTGTGCCATGCCAATGCTATGTCCACCCTTGCCCTCGGCCCCAAGAGTGTCCAGCGGTGGCC  
CACCTCTTCTCCCACTACAGCCTCAACAGTATGTACCATCTCCCACTGTAAATAGTCCCAGTTAGAACGGAATG  
CCGTTGTTTTATAACTTTGAACAAATGTATTTACTGCCCTTCTCAAAA

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**FIGURE 184**

QCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFDS EICGVVSDAVWDAREQQQQILQMAIV  
EHLYQQGMLSVAEELCQESTLNVDLDFKQPFLELNRIEALHEQDLGPALEWAVSHRQRLLEL  
NSSLEFKLHRLHFIRLLAGGPAKQLEALSYARHFQPFARLHQREIQVMMGSLVYLRLGLEKSP  
YCHLLDSSHWAEICETFTRDACSLGLSVESPLSVSFASGCVALPVL MNIAKAVIEQRQCTGVW  
NHKDELPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLCGHVISRDALNKLINGGKCLKCP  
YCPMEQNPADGKRIF

**Transmembrane domain:**

amino acids 222-241

**N-glycosylation site.**

amino acids 129-133

**Tyrosine kinase phosphorylation site.**

amino acids 151-159, 184-193

**Amidation site.**

amino acids 327-331

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 222-233

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**FIGURE 185**

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTAAT  
CTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGC  
TTTGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA  
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCCAGGAACCTGCTCCTGAC  
ATGGCGGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATT  
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC  
CAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCCTCCAAGGATAAAATCAAG  
AACGAACCAAATTAATAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA  
GATTTATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC  
TGTCACAAGCTCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCCTCTGAT  
TGCGGATGCTCTGGACAAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAAGTACTT  
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG  
CAGGTCATACCATGACCGGAAGTCAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG  
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGT  
GGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAACTGT  
CAACTGGAGGTCCTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGTATTACA  
GTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCA  
GTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGT  
GCACATCCTTACATTAAGCCTGAGAGAA

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**FIGURE 186**

MHRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRRDDLYRRDETIQVKNGYVQSPRF  
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEEAENDICRYDFEVEVEDISETSTIIRGRWCG  
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY  
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV  
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQRCGGNCGCGTVNWRSTCNSG  
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 270-274

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 262-266

**Tyrosine kinase phosphorylation site.**

amino acids 256-265

**N-myristoylation sites.**

amino acids 94-100, 186-192, 297-303, 298-304

**TonB-dependent receptor proteins signature 1.**

amino acids 1-56

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**FIGURE 187**

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTTG  
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGGCAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG  
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACACAAAT  
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCTTT  
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT  
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA  
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA  
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGGAGGAGTCCCTCAG  
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT  
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT  
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGAAACGTTACAGTACTCATACACCCC  
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA  
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTTCGCT  
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA  
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAAAACTGATGCCAACA  
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGTCAGTGTCTGTGAGAA

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**FIGURE 188**

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI  
GPPEVALTTDEKSSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRYIHVGKEKHANLILYGNFDRFFVPAEKIVINFITLNISSDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGLTSLTQQESLS  
RTIPDPKTVIEYEDVRTTDICAGPEEQELSLQEEVSTQGTLLSQAALAVLGPQTLQYSYTP  
QLQDLPLAQEHTDSEEGPEEPPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE  
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

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**FIGURE 189**

**ATG**TGCTGCTGGCCGCTGCTCCTGCTGTGGGGGCTGCTCCCCGGGACGGCGGGCGGGGGGCTCG  
GGCCGAACCTATCCGCACCGGACCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGGCTGGAGC  
CAGCGGGGCAGCCAGATCGCCTTCCGCCTCCAGGTGCGCACTGCAGGCTACGTGGGCTTCGGC  
TTCTCGCCACCGGGGCCATGGCGTCCGCCGACATCGTCGTGGGCGGGGTGGCCACGGGCGG  
CCCTACCTCCAGGATTATTTTACAAATGCAAATAGAGAGTTGAAAAAGATGCTCAGCAAGAT  
TACCATCTAGAATATGCCATGGAAAATAGCACACACACAATAATTGAATTTACCAGAGAGCTG  
CATACATGTGACATAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCCTAC  
CACCATGAAGATGCAGGAGAAGCTGGTCCCAAGTACCATGACTCCAATAGGGGCACCAAGAT  
TTGCGGTTATTGAATCCTGAGAAACTAGTGTGCTATCTACAGCCTTACCATACTTTGATCTG  
GTAAATCAGGACGTCCCCATCCCAAACAAAGATACAACATATTGGTGCCAAATGTTTAAGATT  
CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG  
AGTCTGGTGCACCACATCCTGCTCTATCAGTGCAGCAACAACCTTTAACGACAGCGTTCTGGAG  
TCCGGCCACGAGTGCTATCACCCCAACATGCCCGATGCATTCTCACCTGTGAAACTGTGATT  
TTTGCCTGGGCTATTGGTGGAGAGGGCTTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC  
ACTCCATTAGATCCGCATTATGTGCTCCTAGAAGTCCATTATGATAATCCCCTTATGAGGAA  
GGCTTAATAGATAATTCTGGACTGAGGTTATTTTACACAATGGATATAAGGAAATATGATGCT  
GGGGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCATACCATCCCTCCAGGGATGCCTGAG  
TTCCAGTCTGAGGGTCACTGCACTTTGGAGTGCCTGGAAGAGGCTCTGGAAGCCGAAAAGCCA  
AGTGGAATTCATGTGTTTGCTGTTCTTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG  
CGTCATTTTCGAAAAGGGAAGGAAATGAAATTACTTGCCATGATGATGATTTTGACTTCAAT  
TTCCAGGAGTTTCAGTATCTAAAGGAAGAACAACAATCTTACCAGGAGATAACCTAATTACT  
GAGTGTGCTACAACACGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAAGCACCAGGAGT  
GAAATGTGTCTCTCATACCTTCTTTATTACCCAAGAATTAATCTTACTCGATGTGCAAGTATT  
CCAGACATTATGGAACAACCTTCAGTTCATTGGGGTTAAGGAGATCTACAGACCAGTCACGACC  
TGGCCTTTCATTATCAAAAGTCCCAAGCAATATAAAAACCTTTCTTTCATGGATGCTATGAAT  
AAGTTTAAATGGACTAAAAAGGAAGGTCTCTCCTTCAACAAGCTGGTCCTCAGCCTGCCAGTG  
AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGGTCGATTCAAGGAATGACAGCATTACCT  
CCAGATATAGAAAGACCTATAAAGCAGAACCTTTGGTGTGTGGCACGTCTTCTCCTCTTCC  
CTGCACAGAGATTTCTCCATCAACTTGCTTGTTGCCTTCTGCTACTCAGCTGCACGCTGAGC  
ACCAAGAGCTTGT**GAT**CAAAATTCTGTTGGACTTGACAATGTTTTCTATGATCTGAACCTGTC  
ATTTGAAGTACAGGTTAAAGACTGTGTCCACTTTGGGCATGAAGAGTGTGGAGACTTTTCTTC  
CCCATTTTCCCTCCCTCCTTTTTCCTTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT  
CTCTTTCTTAGAAATACCTGATGTTATATATACATGGTCAATAAAATAAACTGGCCTGACTT  
AAGATAACCATTTTAAAAAATTGGGCTGTCATGTGGGAATAAAAGAATTCTTTCTTCTCTAA  
AAAAAAA

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**FIGURE 190**

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLLDSEGKYWLGWSQRGSQIAFRLQVRTAGYVGFG  
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIIEFTREL  
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGTKSLRLLNPEKTSVLSTALPYFDL  
VNQDVPIPNKDTTYWCQMFKIPVFQEKHHVIKVEPVIQRGHESLVHHILLYQCSNNFNDSVLE  
SGHECYHPNMPDAFLTCTETVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEE  
GLIDNSGLRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEALEAEKP  
SGIHVFAVLLHAHLAAGRIRLRHFRKGKEMKLLAYDDDFDNFQEFQYLKEEQTILPGDNLIT  
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT  
WPFIIKSPKQYKNLSFMDAMNKFkWTKKEGLSFNKLVLSPVNVRCSTKDNAEWSIQGMTALP  
PDIERPYKAEPLVCGTSSSSSLHRDFSINLLVCLLLLCTLSTKSL

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 56-73, 378-393, 583-602

**N-glycosylation sites.**

amino acids 114-118, 247-251, 476-480, 517-521

**N-myristoylation sites.**amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,  
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474



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**FIGURE 191**

GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTTTGTTCCTTTATAACAT  
TTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAAAATGAAGAAAATATGCAACTGGCTCAGG  
CATATCTCAACCAGTTCTACTCTCTTGAATAGAAGGGAATCATCTTGTTCAAAGCAAGAATA  
GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGACAGTGACTGGAA  
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCC  
AGTATGGCTACACCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAAACTATA  
CTCCGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGCA  
AAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTTA  
GGACTCGAGTCCATGGTCGGTGTCCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG  
CCTTTCCTCCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAACCTGGACCA  
AGGATGGAGCAGGATTCAACTTGTTTCTTGTGGCTGCTCATGAATTTGGTCATGCACTGGGGC  
TCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAA  
AATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG  
TACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCTGACTTGACTTTTGACG  
CTATCACAACTTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATT  
ATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTCTGGCCATCTCTGCCAGCTGATC  
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGA  
TGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAG  
GACGTGTGAAGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAAACCTACTTCTTTG  
TGGGCATTTGGTGCTGGAGGTTTGTATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA  
GAGTGGTAAAACACTTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTTCAGTACAAAGGAT  
TCTTCTTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAAAGAATATTACCC  
GAATCATGAGAATAATACTTGGTTTCAATGCAAAGAACCAAAGAACTCCTCATTTGGTTTTG  
ATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCT  
TGTTTATTTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTTATCATAAATTCATAGAC  
CTAAAATAAACCTCAACAGGTCTTTTAATATAAATTCTGCTTCAAATAGATAAAACCATTC  
TTTAAACAAC

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**FIGURE 192**

MKRLLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLLDDKI  
REMQAFFGLTVTGKLDSENTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTIRIINYTPDMARAA  
VDEAIQEGLEVWSKVTPFKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFPPGPGL  
GGDTHFDEDENWTKDGAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDD  
INGIQSIYGGLPKVPAKPKEPTIPHACDPDLTFDAITTFRREVMFFKGRHLWRIYYDITDVEF  
ELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA  
AVCDKTTRKTYFFVGIWCWRFDGMTQMDKGFPQRVVKHFPGISIRVDAAFQYKGFFFFSRGS  
KQFEYNIKTKNITRIMRTNTWFQCKEPPKSSFGFDINKEKAHSGGIKILYHKSLSLFI FGIVH  
LLKNTSIYQ

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

**N-myristoylation site.**

amino acids 71-77, 205-211, 223-229

**Hemopexin domain signature.**

amino acids 171-202, 207-238, 318-334

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 213-223

**Matrixins cysteine switch.**

amino acids 89-97, 207-238

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**FIGURE 193**

CACAATCAGGTCCCATTCTATAGATGGGGAAACTGAGGCTTGAGGTCACATAGGCGTCGTTCA  
AGGCTGGTATACCTGCACCCTCTCCCATGTGAACAACATGGTTCTGGGTAATGGGGGCTGTCA  
TCCAGTCTCCTCCCTGCCCCCTGCTGGTGCACTTCCTGCCTCTGCTGGTGCACTTTCTGCCCCCT  
ACTGGTATATTTGCTGCCTCTGCTGGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCCCT  
GCTGGTGCACTTTCTGCCCCCGCTGATGCACTTCCTGCCTCTGCTGGTGCACTTCCTGGCTCT  
GCTGGCACACTTCCTGCCTCTGCTGGTGCACTTCCTGGCTCTGCTGGCGCACTTTCCTGCCCC  
TGCTGGTGTATTTCTGCCCCCTGCTGGTGTACTTCCTTCCCCTGCTGGTGCACTTCCTGCCTC  
TGCTGGCGCACTTCTTGCTCTCCAGGCCCTACCTTAGCCTCTCCCTCTTATATATGGAAGTCT  
TCCCAGTTCACTGACACTGGTAACAGGGACTCTGCTCTTGGTGTTGCTGTCTGCCCTGGGGAT  
GGGCATCTGTGTCTTCCTTTACTACTGCTGGCTCAGGACCCAGAGCTTTGAAGCATGTCCAGA  
TGCAGGTCCGGGCACCAGAGTCTAAGGAGCCCCTACACCCACCAGGATTTTCCAATAAAGAGA  
TGTTACCA

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## **FIGURE 194**

MVLGNGGCHPVSSLPLL VHFLPLL VHFLPLL VYLLPLL GRFLPRL VYLLPLL VHFLPPL MHFL  
PLL VHFLALL AHFLPLL VHFLALL AHFPAPAGVFPAPAGVLPSPAGALPASAGALLASPGPT

**Signal peptide:**

amino acids 1-39

**N-myristoylation sites.**

amino acids 4-10, 109-115, 116-122

**Leucine zipper pattern.**

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,  
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,  
65-87, 66-88

[illegible]

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**FIGURE 196**

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPQVQTPKPSDADWDDLWDQFDERRYLN  
AKKWRVGGDPYKLYAFNQRESERISSNRAIPDTRHLRCTLVYCTDLPPTSIIITFHNEARST  
LLRTIRSVLNRTPTHLIREIILVDDFSNDPDDCKQLIKLPVKCLRNNERQGLVRSRIRGADI  
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWS  
LHFQWEQLSPEQKARRLDPTPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFR  
VWMCGLSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDYKQYYYAARPFAL  
ERPFNGVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLSQQRQNNQET  
PNLKLSPCAKVKGEDAKSQVWAFYTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK  
TGSHEHIAHLCLDMDFGDGTENGKEIVVNPCESSLMSQHWDMVSS

**Transmembrane domain:**

amino acids 475-493

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-6

**Tyrosine kinase phosphorylation sites.**

amino acids 68-75, 401-409

**N-myristoylation sites.**

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

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**FIGURE 197**

GCAGCTCACCTTTCGCAGCCGCGATGGGGGAAGACGACGCCGCGCTTCGGGCTGGCAGCAGGGGGCTCTCCGACC  
CGTGGGCAGACTCAGTGGGAGTGCAGCCCCGCCACCGAGCGCCACATCGCCGTACACAAGCGGCTTGTGCTGG  
CCTTCGCTGTGTCCCTCGTGGCATTGCTCGCGGTACAATGCTCGCTGTGCTGCTCAGCCTGCGCTTCGACGAGT  
GCGGGGCGAGTGCCACGCCAGGCGCCGACGGTGGCCCCCTCAGGCTTTCGGAGCGCGGCGGCAACGGGAGCCTCC  
CTGGATCGGCCCGCGCAACCACCACGCAGGCGGGGACTCCTGGCAGCCGAGGCGGGTGGGGTGGCCAGTCCGG  
GGACCACGTCGGCCAGCCGCGCTCGGAGGAGGAGCGGGAGCCGTGGAGCCGTGGACGCGAGCTGCGCCTGTCCG  
GCCACCTGAAGCCGCTGCACTACAATCTGATGCTCACCGCCTTCATGGAGAAGCTTCACCTTCTCGGGGAGGTCA  
ACGTGGAGATCGCGTGCCGGAACGCCACCCGCTACGTAGTGTGCACGCTTCCCGAGTGGCGGTGGAGAAAGTGC  
AGCTGGCCGAGGACCGGGCGTTCGGGGCTGTCCCTGTAGCCGGTTTTTTTCTCTACCCGCAAACCCAGGTCTTAG  
TGGTGGTGTGAATAGGACACTGGACGCGCAGAGGAATTACAATCTGAAGATTATCTACAACGCGCTCATCGAGA  
ATGAGCTCCTGGGCTTCTTCCGAGCTCCTATGTGCTCCACGGGGAGAGAAGATTCTTGGTGTACTCAGTTTT  
CGCCTACACATGCCAGAAAGGCATTTCTTGTGTTGATGAGCCAAATCTACAAGGCTACTTTCAAATCAGCATCA  
AGCATCAAGCAACCTATTTATCTTTATCTAATATGCCAGTGGAACTTCCGTGTTTGGGAAGATGGATGGGTTA  
CGGATCACTTTTTCACAGACCCCTCTCATGTCCACATATTATTTAGCCTGGGCAATTTGCAACTTCACATACAGAG  
AAACTACCACCAAGAGTGGGGTGTAGTACGATTATATGCAAGACCTGATGCTATCAGAAGAGGATCCGGGGACT  
ATGCTCTCCATATAACAAAGAGATTAATAGAAATTTATGAAGACTACTTTAAAGTGCCCTATTCTTGC AAAAC  
TAGATCTTTTAGCTGTGCCAAGCATCCGTATGCTGCTATGGAGAAGTGGGGACTAAGTATTTTGTGGAACAAA  
GAATACGCTGGATCCAGTGTTCATCTATTCTTATTTGCTGGATGTCACCATGGTCATTGTTTCATGAGATAT  
GTCACCAAGTGGTTTGGTGACCTTGTGACGCGCTGTGTTGGGAAGACGTGTGGCTGAAGGAAGGGTTTGCTCACT  
ACTTTGAATTTGTTGGTACAGACTACCTCTATCCTGGCTGGAACATGGAAAAGCAGAGGTTTCTGACCGATGTTT  
TGCATGAAGTGATGCTGCTGGACGGTTTGGCCAGTTCCTCATCCAGTATCACAGGAAGTGTGTCAGGCAACAGATA  
TTGACAGGGTGTGTTGACTGGATCGCATATAAAAGGGTGTGCTTTAATAAGAATGCTGGCTAATTTTATGGGCC  
ATTGAGTTTTCCAGAGGGGTTTGAAGATTATTTAAACATTTCATAAGTATGTAATGCAGCCAGAAATGATCTCT  
GGAATACATTATCGGAGGCTTTAAAAAGAAATGGGAAATATGTAATATACAGAAGTAATGGATCAGTGGACAC  
TCCAGATGGGTTATCCTGTTATCACCATCTTGGGAAACACAACAGCAGAAATAGAATAATAATTACCCAACAGC  
ATTTTATCTATGATATCAGTGCTAAACTAAAGCACTTAACTTCAGAATAACAGTTACCTGTGGCAGATTCCAT  
TAACTATTGTGGTAGGAAATAGAAGCCATGTGCTTCAGAAGCAATTATTTGGGTGTCTAACAAATCAGAGCACC  
ACAGAATAACTTATTTGGACAAAGGAAGCTGGCTGCTGGGGAACATCAATCAAAGTGGCTATTTTAGAGTCACT  
ATGACCTAAGGAAGTGGAGATTATTAATTGATCAATTAATCCGGAATCATGAGGTTCTTTCTGTCAAGTACCGGAG  
CGGGCTTGATCGATGATGCCTTCAGCCTAGCCAGGGCTGGCTATTTGCCTCAGAATATTTCTCTGGAGATTATCA  
GATACCTGTCTGAGGAGAAGGATTTTCTTCTTGGCATGCTGCCAGCCGAGCTCTTATCTCTAGATAAATTAC  
TGGACCGCATGGAAAACATAACATTTTCAATGAATATATTTTAAAGCAAGTTGCAACAACATATATCAAGCTTG  
GGTGGCCGAAAAATAATTTTAAATGGATCTCTTGTCAAGCATCTACCAACATGAAGAACTACGTAGAGAAGTTA  
TAATGCTGGCCTGCAGTTTTGGCAACAAGCACTGTCAACAACAGGCATCAACACTTATTTAGATTGGATTTCCA  
GCAACAGGAACAGAATACCATAAATGTTAGAGACATCGTACTGTACAGGAGTGTCACTAGTGGATGAGGATG  
TCTGGGAATTCATATGGATGAAATTCATTTCCACCACAGCAGTCTTCTGAGAAGAAAATATTATTGGAAGCCTTAA  
CTTGCAAGTGTGACAGGAATTTATTAACAGGCTTCTAATCTGTCACTGAATCTGAGGTGGTGTGCTGGATCAAG  
ATGCAATTGATGTCATAATCCATGTAGCTCGAAATCCACATGGTTCGAGACCTTGCCTGGAAGTTTTTCAGGGATA  
AATGGAAGATATTAATACCAGGTATGGAGAAGCATTGTTTATGTATTCCAACTCATCAGTGGTGTACAGAAAT  
TTCTTAATACTGAAGGTGAAGTCAAAGAGCTCAAGAACTTCATGAAAACTATGATGGGGTAGCTGCTGCTCTCT  
TCTCACGAGCTGTGGAACTGTGCAAGCCAATGTGCGCTGGAAAATGCTTTACCAAGACGAGCTTTTCCAATGGT  
TAGGAAAAGCTCTAAGACACTAATATATGTATCTTATAAACAAACAATTCAACTCAGAAGTTTATGAGAAGACAC  
GCTTTTTGTGGAATGAGGAAAATGTACTACCTAGAAAATGGCCAGATTTTCAGTGTTAACGTGTGGGAGGAATTT  
TTTTTTTTTAGTTTTTATTTTTTGGTTTTGGGGGATATTTTTTATTTGTTTCATTCTGTTCTGTTTCTCTAC  
TGGGTGTTCTCTCTAAAGAACTCTTGCAAGTGAACTAGCCATGATTGCTTCAGCTGTACATTCTTGTGCTGTA  
CAGGACCAATATGATAGTGATGCATGTTGATGTTACAGTCAATTTGGAAAAACATATTCAGAATATCTGTGCAT  
GGATATATTGCTGCTGTGTTCCAGCATGCTTATTTCAAACGTCAGTGTGTTGTGTGAATATGTGTTACACC  
TAGGATGGGCATTATGCAAAAGCACAAAGATTATATATGCAATCAGTATTGCAATGAAAGAAAACTAAAAACA  
GAAATGATATTCTCAATTTTGGGCAATGTGAGAGGTAAAATAGCCCTTGACATGATGAACATCACTTATTTTCAGC  
ACTTGGATTGTCTGGCAATGATTACTGTGTTGCTAACTCATTTTCTTTGAGTTAAAGCTGTGTATACATTTTAAA  
AGGCATATAGATAGTGTATGCATATGTATATGTACATAGGGAAGCCCCATATGTATATAGTATGTTGTACACTGC  
ACATGTACAAAGATGTCTTCAGATCAAAGAAAATTTATCTCTTTTATAAACTTAAGGACAGTTGCAAAAGGCT  
TCAAGGAATTTTCAACATTTCTTCTATGTCTCAACTAAATTTCTCACTGTATGAATTTTCTCATCTAC  
TTCTTGAACAGTGGTCTATTCTGCTACATGAAGATGAATACAAACAAAATTTTGTATAAACTCCCAAAAAAAA  
AAAAA

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**FIGURE 198**

MGEDDAALRAGSRGLSDPWADSVGVRPRTERHIAVHKRLVLFAVSLVALLAVTMLAVLLSL  
RFDECGASATPGADGGPSGFPERRGGNGSLPGSARRNHAGGDSWQPEAGGVASPGTTSAQPPS  
EEEREFPWEPWTQLRLSGHLKPLHYNLMLTAFMENFTFSGEVNVEIACRNATRYVVLHASRVAV  
EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKIIYNALIENELLGFFRSS  
YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG  
WVTDHFSQTPLMSTYYLAWAICNFTYRETTTKSGVVVRLYARPD AIRRGSGDYALHITKRLIE  
FYEDYFKVPYSLPKLDLLAVPKHPYAAMENWGLSIFVEQRILLDPSVSSISYLLDVTMVIVHE  
ICHQWFGDLVTPVWVEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLTDVLHEVMLLDGLAS  
SHPVSQEV LQATDIDRVFDWIAYKKGAALIRMLANFMGHSVFQRLQDYLT I HKYGNAARNDL  
WNTLSEALKRNGKYVNIQEVMQWTLQMGYPVITILGNTTAENRIIITQQHFIYDISAKTKAL  
KLQNNSYLWQIPLTIVVGNRSHVSSEAIIWVSNKSEHHRITYLDKGSWLLGNINQTYFRVNY  
DLRNWRLLDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNI PLEIIRYLSEEKDFLPWHA  
ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNNFNGLSVQASYQHEELRREVIM  
LACSFGNKHCHQQASTLISDWISSNRNRIPLNVRDIVYCTGVSLLEDVWEFIWMKFHSTTAV  
SEKKILLEALTCSDDRNLLNRLNLSLNSEVVLDQDAIDVIIHVARNPHGRDLAWKFFRDKWK  
ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAASFSRAVETVEANVRWKM  
LYQDELFQWL GKALRH

**Transmembrane domain:**

amino acids 44-63

**N-glycosylation sites.**amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,  
634-638, 649-653, 663-667, 684-688, 800-804, 906-910**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 362-366

**Tyrosine kinase phosphorylation site.**

amino acids 520-528

**N-myristoylation sites.**amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,  
825-831, 987-993**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 437-447



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**FIGURE 199**

GCGCCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGCGTCCGCCCAGGGGGCTCCGGAAGCTGCCCC  
GGCCCGCGGCTCCTCCCTCGCTCCCGCTTCCCTTTCTCGCTACCGCCGCCCTCCTTCCCCAGCTCCCTCGCC  
GTCCGCCCGCCCCACAGCCAGCGGCTCCGCGCCCCCTGCAGCCACGATGCCCGCGGCCCGGCCCGCCGCGGG  
ACTCCGCGGGATCTCGCTGTTCTCGCTCTGCTCCTGGGGAGCCCGCGGCAGCGCTGGAGCGAGATGCTCTTCC  
CGAGGGAGATGCTAGCCCTTTGGGTCTTACCTCCTGCCCTCAGGAGCCCCGGAGAGAGGAGTCTGGCAAAGA  
GCACCCTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTCTCACAGTCGGCGGAAGTGTGGGCGAGCTGGTGTCT  
GGATGGGACCGCACCTCTGCACATCACGACATCCAGCCCTGTACCGCTGCTTCCAGAGGAGGCCCGCCCCAA  
GCACGCCTTGCCCCCAAGAAGAACTGCCTTCGCTCAAGCAGGTGAACCTGCCAGGAAGCAGCTGAGGCCCAA  
GGCCACCTCCGCAGCCACTGTCAAAGGGCAGGGTCCCAGCCAGCGTCCCAGGGCCTAGATCTCCTCTCCTCCTC  
CACGGAGAAGCCTGGCCACCGGGGGACCCGACCCCATCGTGGCCTCCGAGGAGGCATCAGAAGTGCCCTTTG  
GCTGGATCGAAAGGAGAGTGGCGTCCCTACAACACCCGCACCCCTGCAAATCTCCCCCTTCACTTCGCAGCCCTA  
TGTGGCCACACACTCCCCAGAGGCCAGAACCCGGGGAGCCTGGGCCTGACATGGCCAGGAGGCCCCCCAGGA  
GGACACCAGCCCCATGGCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGA  
GACCACTACCTCCACCATATCACCACCACGGTCATCACCACCGAGCAAGCACCAGCTCTCTGCAGTGTGAGCTT  
CTCCAATCCTGAGGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTCAACAACTTTCTGGAGTGCACATA  
CAACGTGACAGTCTACACTGGCTATGGGGTGGAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGT  
CTCCATCCGCGGGGTGGACGGCCCTACCTGACCGTCTGGCCAACCAGACACTCCTGGTGGAGGGGCAGGTAAT  
CCGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGGCTTGGGACCTTCCAGCTTCA  
CTACCAGGCCTTTCATGCTGAGCTGCAACTTTCCCGCGGGCCTGACTCTGGGGATGTACGGTGTGGACCTGCA  
CTCAGGTGGGGTGGCCCACTTTCACTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAA  
TGCCTCCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGCAGTGCACAATGCCAC  
CATCGGCCCGCTCCTTCCCCAAGTTACCCTGAAACACAAATGGGAGCCAATTCTGCATCTGGACGATTGAAGC  
TCCAGAGGGCCAGAAGCTGCACCTGCACCTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCACAG  
CGGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTTGAGGGCCTGCTGAG  
CGAAGGCAACACCATCCGCATCGAGTTCACGTCCGACCAGGCCCGGGCGGCCCTCCACCTTCAACATCCGATTTGA  
AGCGTTTGAGAAAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACCTTCACTACATCCGACCCGACCTATAA  
CATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCCGGCCATCATCGAATGCAT  
CAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGTGGGGAGCTCTCTGCTGT  
GGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGT  
GGGAGAAGAGAAACGGATCTTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGA  
TGGCGACGAGGTGATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCCTCCAC  
GCCAGACTTAACCATCCAGTTCATTCCGACCCTGCTGGCCTCATCTTGGAAAGGGCCAGGGATTTATCATGAA  
CTACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCA  
CACGGAGTTGGTGGGGGAGCCAGAATCACCTACCAGTGTGACCCCGGCTATGACATCGTGGGGAGTGACACCT  
CACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCATTTTGTGAGAAAATTATGTACTGCACCCGACCCCG  
AGAGGTGGATCACTCGACCCGCTTAATTTGGATCCTGTGCTGGTGGGGACCACTCCAATACACCTGCAA  
CCCCGGTTTTGTGCTTGAAGGGAGTTCTCTTCTGACCTGCTACAGCCGTGAACAGGGACTCCCATCTGGACGTC  
TCGCCTGCCCCACTGCGTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAAAATGGATACCAAT  
CCTGTACAAGCGACTTACCTGCCAGGAGAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGA  
AGTGACCATCCGCTGCATCCTGGGACAGCCATCCCACTGGAACGGGGCCCTGCCCGTGTGTAAAGTTAATCAAGA  
CAGTTTTGAACATGCTTTAGAAGCAGAAGCGGCAGCAGAGACGTCGCTGGAAGGGGGGAACATGGCCCTGGCTAT  
CTTCATCCCGGTCCTCATCATCTTACTGCTGGGAGGAGCCTACATTTACATCACAAGATGTGCTACTATTTC  
CAACCTCCGCCTGCCTCTGATGTACTCCACCCCTACAGCCAGATCACCGTGGAAACCGAGTTTGACAACCCCAT  
TTACGAGACAGGGGAAACAGAGAGTATGAGTTTCTATCTAAAGAGAGCTACACTTGAGAAGGGGACTTGTGAA  
CTCAACCACAATCTCCTCGAGACATTATCCAGAGACCATGTGGCACTTGATTGAAACCCAGAAATGTGCACTGT  
CTTTTGTGTAGACTCTTTATCAAAGGTTTACTGTTTTCTCCCTGTATTTATTATATTTAAAGTGAAAAA  
AAAAA

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**FIGURE 200**

MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE  
ERVVTAPPSSSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPEEARPKHALPPKKKLPSLKQVN  
SARKQLRPKATSAATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPVASEEASEVPLWLDRK  
ESAVPTTPAPLQISPFTSQPYVAHTLPQRPEPGEPGDMAQEAPQEDTSPMALMDKGENELTG  
SASEESQETTTSTIITTTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNNFLECTYNVTYV  
TGYGVELQVKS VNLS DGELLSIRGVDGPTLTVLANQTLLVEGQVIRSPTNTISVYFRTFQDDG  
LGT FQLHYQAFMLSCNFPRRPDSGDVTVM DLHSGGVAHFHCHLGYELQGAKMLTCINASKPHW  
SSQEPICSA PCGGAVHNATIGRVLSPSY PENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD  
RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGN TIRIEFTSDQARAASTFNIRFEAFEKGHC  
YEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGP AII ECINVRDPYWNDEPLCRAMCGG  
ELSAVAGVVLSPNWPEPYVEGEDCIWKI HVGEEKRIFLDIQFLNLSNSDILTIYDGDEVM PHI  
LGQYLGN SGPQKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYIEVSRNDSCSDLPEIQNGWK  
TTSHTELVRGARITYQC DPGYDIVGSDTLTCQWDL SWSSDPFCEKIMYCTDPGEVDHSTR LI  
SDPVLLVGT TIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDN PGLPENG  
YQILYKR LYLPGESLTFMCYEGFELMGEVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA  
AAETSLEGGNMALAI FIPVLIISLLLGGAYIYITRCRYYSNLRLPLMYSHPY SQITVETEFDN  
PIYETGETREYEVS I

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 893-915

**N-glycosylation sites.**amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,  
514-518, 576-580, 618-622, 674-678, 742-746**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

**N-myristoylation sites.**amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,  
629-635, 695-701, 723-729, 766-772, 877-883, 953-959**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

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**FIGURE 201**

GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGGAAGTCGGGGTCTCCTTCGCCTTCT  
GTCTTTTCTGCGTCCCTACTAGCAGGTTTGTGCGAGGGGAACTCAGTGGAGAGGAAGATATATAT  
CCCCTTAAATAAAACAGCTCCCTGTGTTCGCCTGCTCAACGCCACTCATCAGATTGGCTGCCA  
GTCTTCAATTAGTGGAGACACAGGGTTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTG  
GGTATTGACTGATGGCCCCAACCCCCCTTACATGGTTCTGCTGGAGAGCAAGCATTTTTACCAG  
GGATTTAATGGAGAAGCTGAAAGGGAGAACCAGCCGAATTGCTGGTCTTGCAGTGTCTTGAC  
CAAGCCCAGTCTGCCTCAGGCTTCTCTCCTAGTGTACAGTGCCCAAATGATGGGTGTTGGTGT  
TTACTCCAATTCCTATGGGCCAGAGTTTGTCACTGCAGAGAAATACAGTGGAAATTCGCTGGG  
CAATGGTTTGGCTTATGAAGACTTTAGTTTCCCCATCTTTCTTCTTGAAGATGAAAATGAAAC  
CAAAGTCATCAAGCAGTGCTATCAAGATCACAACCTGAGTCAGAATGGCTCAGCACCAACCTT  
CCCCTATGTGCCATGCAGCTCTTTTCACACATGCATGCTGTCATCAGCACTGCCACCTGCAT  
GCGGCGCAGTCCATCCAAAGCACCTTCAGCATCAACCCAGAAATCGTCTGTGACCCCTGTCTC  
TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACAACCTGGGACATTAAAGCCTGACGA  
CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTTCTTTTCTGGAATGTGGCCCCAGG  
GGCTGAAAGCGCAGTGGCTTCTTTGTACCCAGCTGGCTGCTGCTGAAGCTTTGCAAAGGC  
ACCTGATGTGACCACCTGCCCGCAATGTCATGTTTGTCTTCTTTCAAGGGGAACTTTTGA  
CTACATTGGCAGCTCGAGGATGGTCTACGATATGGAGAAGGGCAAGTTTCCCGTGCAGTTAGA  
GAATGTTGACTCATTTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTCATTAGAGCTTTGGAT  
GCACACAGATCCTGTTTCTCAGAAAAATGAGTCTGTACGGAACCAGGTGGAGGATCTCCTGGC  
CACATTGGAGAAGAGTGGTGTGCTGGTGTCCCTGCTGTATCCTCAGGAGGCCAAATCAGTCCCA  
GCCTCTCCACCATCTTCCCTGCAGCGATTTCTTCGAGCTCGAAACATCTCTGGCGTTGTTCT  
GGCTGACCACTCTGGTGCCTTCCATAACAAATATTACCAGAGTATTTACGACACTGCTGAGAA  
CATTAAATGTGAGCTATCCCGAATGGCTGAGCCCTGAAGAGGACCTGAACCTTTGTAACAGACAC  
TGCCAAGGCCCTGGCAGATGTGGCCACGGTGTGGGACGTGCTCTGTATGAGCTTGCCAGGAGG  
AACCAACTTCAGCGACACAGTTCAGGCTGATCCCCAAACGGTTACCCGCCTGCTCTATGGGTT  
CCTGATTAAAGCCAACAACCTCATGGTTCCAGTCTATCCTCAGGCAGGACCTAAGGTCCTACTT  
GGGTGACGGGCCTCTTCAACATTACATCGCTGTCTCCAGCCCCACCAACACCACTTATGTTGT  
ACAGTATGCCTTGGCAAATTTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCCAGGA  
TCCAAGTAAAGTCCCAAGTGAACAAGGATCTGTATGAGTACTCATGGGTCCAGGGCCCTTT  
GCATTCTAATGAGACGGACCGACTCCCCCGGTGTGTGCGTTCTACTGCACGATTAGCCAGGGC  
CTTGTCTCCTGCCTTTGAACTGAGTCAGTGGAGCTCTACTGAATACTCTACATGGACTGAGAG  
CCGCTGGAAAGATATCCGTGCCCGGATATTTCTCATCGCCAGCAAAGAGCTTGAGTTGATCAC  
CCTGACAGTGGGCTTCGGCATCCTCATCTTCTCCCTCATCGTCACCTACTGCATCAATGCCAA  
AGCTGATGTCCTTTTCATTGCTCCCCGGGAGCCAGGAGCTGTGTCATACTGAGGAGGACCCCA  
GCTTTTCTTGCCAGNTCAGCAGTTCACCTTCTAGAGCATCTGTCCCACTGGGACACAACCACT  
AATTTGTCACTGGAACCTCCCTGGGCCTGTCTCAGATTGGGATTAACATAAAAGAGTGGAAC  
ATCCAAAAGAGACAGGGAGAAATAAATAAATTGCCTCCCTTCTCCGCTCCCTTTCCCATCA  
CCCCTTCCCCATTTCTCTTCTTCTACTCATGCCAGATTTTGGGATTACAAATAGAAGCT  
TCTTGCTCCTGTTTAACTCCCTAGTTACCCACCCTAATTTGCCCTTCAGGACCCTTCTACTTT  
TTCCTTCTGCCCCTGTACCTCTCTGCTCCTCACCCCCACCCCTGTACCCAGCCACCTTCTCT  
GACTGGGAAGGACATAAAAGGTTTAAATGTCAGGGTCAAACCTACATTGAGCCCTGAGGACAGG  
GGCATCTCTGGGCTGAGCCTACTGTCTCCTTCCCACTGTCTTTCTCCAGGCCCTCAGATGGC  
ACATTAGGGTGGGCGTGTGCGGGTGGGTATCCACCTCCAGCCACAGTGCTCAGTTGTACT  
TTTTATTAAGCTGTAATATCTATTTTTGTTTTGTCTTTTCTTTTCTTTTGTAAATAT  
ATATATAATGAGTTTCATTAAATAGATTATCCC

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**FIGURE 202**

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCQ  
SSISGDTGVIHVVEKEEDLQWVLTGPNPPYMVLESKHFTRDLMKLGRTSRIAGLAVSLT  
KPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLDENET  
KVIKQCYQDHNLSQNGSAPTFLCAMQLFSMHAVISTATCMRRSSIQSTFSINPEIVCDPLS  
DYNVWSMLKPINTTGTLPDDRNVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKA  
PDVTTLPARNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM  
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFLRARNISGVVL  
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFEVTD TAKALADVATVLGRALYELAGG  
TNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLG DGPLQHYIAVSSPTNTTYVV  
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA  
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK  
ADVLFIAPREPGAVSY

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 671-692

**N-glycosylation sites.**

amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,  
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,  
573-577, 580-584, 612-616

**Glycosaminoglycan attachment site.**

amino acids 404-408

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 232-236

**N-myristoylation site.**

amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,  
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

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**FIGURE 203**

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCGGAAACCCTGCCAGGGGAGCCGGGTTTT  
GAGCTCAGGCGCCTCTAGCGGCGGCCCCAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA  
CTGAATAGCAAACCTGAGGCTGAGTAGGGAACAGACC**ATG**AGGTCAGTGCAGATCTTCCTCTCC  
CAATGCCGTTTGCTCCTTCTACTAGTTCCGACAATGCTCCTTAAGTCTCTTGGCGAAGATGTA  
ATTTTTACCCCTGAAGGGGAGTTTGACTCGTATGAAGTCACCATTCTGAGAAGCTGAGCTTC  
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCCGTGTCTACCTACTGCAGTTAAAAGGCAAGAAG  
CACGTCCTCCATTTGTGGCCCAAGAGACTTCTGTTGCCCCGACATCTGCGCGTTTTCTCCTTC  
ACAGAACATGGGGAACCTGCTGGAGGATCATCCTTACATAACAAAGGACTGCAACTACATGGGC  
TCCGTGAAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGGTCTCCGAGGT  
GTATTTAACATTGATGCCAAACATTACCAAATTGAGCCCCCTCAAGGCCCTCTCCAGTTTTGAA  
CATGTCGTCTATCTCCTGAAGAAAGAGCAGTTTGGGAATCAGGTTTGTGGCTTAAGTGATGAT  
GAAATAGATGGCAGATGGCCCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCTGGATCC  
TATAAACACCCAAAGTACTTGGGAATTGATCCTACTCTTTGATCAAAGTAGGTATAGGTTTTGTG  
AACAACAATCTTTCTCAAGTCATACATGATGCCATTCTTTTGACTGGGATTATGGACACCTAC  
TTTCAAGATGTTTCGTATGAGGATACACTTAAAGGCTCTTGAAGTATGGACAGATTTTAAACAA  
ATACGCGTTGGATATCCAGAGTTAGCTGAAGTTTTAGGCAGATTTGTAATATATAAAAAAAGT  
GTATTAAATGCTCGCTGTCTCAGATTGGGCACATTTATATCTTCAAAGAAAATATAATGAT  
GCTCTTGCATGGTCGTTTGGAAAAGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA  
CTAGATACAAATATCCTTGCCCTGCTACCTGGTCTGCTCATGAGCTGGGTCATGCTGTAGGA  
ATGTCACATGATGAACAATACTGCCAATGTAGGGGTAGGCTTAATTGCATCATGGGCTCAGGA  
CGCACTGGGTTTAGCAATTGCAGTTATATCTCTTTTTTAAACATATCTCTTCGGGAGCAACA  
TGTCTAAATAATATCCAGGACTAGGTTATGTGCTTAAGAGATGTGGAAACAAATTTGTGGAG  
GACAATGAGGAATGTGACTGTGGTTCCACAGAGGAGTGTGAGAAAGATCGGTGTTGCCAATCA  
AATTGTAAGTTGCAACCAGGTGCCAAGTGTAGCATTGGACTTTGCTGTCATGATTGTGCGGTTT  
CGTCCATCTGGATACGTGTGTAGGCAGGAAGGAAATGAATGTGACCTTGACAGTACTGCGAC  
GGGAATTCAAGTTCTGCCCCAATGACGTTTATAAGCAGGATGGAACCCCTTGCAAGTATGAA  
GGCCGTTGTTTTCAGGAAGGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTTTTGGACCT  
GATGCCATGGAGGCTCCTAGTGAGTGCTATGATGCAGTTAACTTAATAGGTGATCAATTTGGT  
AACTGTGAGATTACAGGAATTCGAAATTTTTAAAAAGTGTGAAAGTGCAAATTCATATGTGGC  
AGGCTACAGTGATAAATGTTGAAACCATCCCTGATTTGCCAGAGCATACGACTATAATTTCT  
ACTCATTTACAGGCAGAAAATCTCATGTGCTGGGGCACAGGCTATCATCTATCCATGAAACCC  
ATGGGAATACCTGACCTAGGTATGATAAATGATGGCACCTCCTGTGGAGAAGGCCGGGTATGT  
TTTAAAAAAATTGCGTCAATAGCTCAGTCTGAGTTTACTGTTTGCCTGAGAAATGCAAT  
ACCCGGGGTGTGTTGCAACAACAGAAAAAACTGCCACTGCATGTATGGGTGGGCACCTCCATTC  
TGTGAGGAAGTGGGGTATGGAGGAAGCATTGACAGTGGGCCTCCAGGACTGCTCAGAGGGGCG  
ATTCCCTCGTCAATTTGGGTGTGTCCATCATAATGTTTCGCCTTATTTTATTAATCCTTTCA  
GTGGTTTTTGTGTTTTTCCGGCAAGTGATAGGAAACCACTTAAACCCAAACAGGAAAAAATG  
CCACTATCCAAAGCAAAAACCTGAACAGGAAGAATCTAAAACAAAACCTGTACAGGAAGAATCT  
AAAACAAAACCTGGACAGGAAGAATCTGAAGCAAAAACCTGGACAGGAAGAATCTAAAGCAAAA  
ACTGGACAGGAAGAATCTAAAGCAAAACATTGAAAGTAAACGACCCAAAGCAAAGAGTGTCAAG  
AAACAAAAAAGT**TAA**CCGGGCAATCCATACTCATTCAGTAACACAGGCTCATTTATTTAACCA  
GCTAATCATTTATCCAAAGGCTTTCCATTCTTCTCCCAATATTTTTTTTACTTTAATTTTTCCC  
ACAAGTTTTGATCAGCAAATAAACAGCATTCTTGTTTTGGAAACAAAA

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**FIGURE 204**

MRSVQIFLSQCRLLLLLVPTMLLKSLGEDVIFHPEGEFDSYEVTIPEKLSFRGEVQGVVSPVS  
YLLQLKGKKHVLHLWPKRLLLPRHLRVFSFTEHGELLEDPYIPKDCNYMGSVKESLDSKATI  
STCMGGLRGVFNIDAKHYQIEPLKASPSFEHVYLLKKEQFGNQVCGLSDDEIEWQMAPYENK  
ARLRDFPGSYKHPKYLELILLFDQSRVRFVNNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA  
LEVWTDNFNKIRVGYPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDALAWSFGKVCSL  
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGLNLCIMGSGRTGFSNCSYISF  
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDGCGSTEECQKDRCCQSNCKLQPGANCSI  
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTPCKEYEGRCFRKGCRSRY  
MQCQSIFGPDAMEAPSECYDAVNLIQDQFGNCEITGIRNFKKCESANSICGRLQCINVTIPD  
LPEHTTIIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNVCNSSLVQ  
FDCLPEKCNTRGVCNNRKNCHCMYGWAPPFCEEVGYGGSIDSGPPGLLRGAIPSSIWVVSIIIM  
FRLILLILSVVFVFFRQVIGNHLKPKQEKMPLSKAKTEQEESKTKTVQEESKTKTGQEESEAK  
TGQEESKAKTGQEESKANIESKRPKAKSVKKQKK

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 684-705

**N-glycosylation sites.**

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

**N-myristoylation sites.**amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,  
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,  
758-764, 767-773**Amidation site.**

amino acids 69-73

**Disintegrins proteins**

amino acids 429-479

**EGF-like domain proteins**

amino acids 650-662

**Neutral zinc metallopeptidases, zinc-binding region proteins**

amino acids 335-345

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**FIGURE 205**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGGAAGGTTGAATGGGGTAGAAGGCCTG  
TTGTGGAGGGAACCAACCATCCTCCTGCCTCCCACCACCACCATCATCCTGGCTGGACGGAG  
AGGGTGACGGGGGCTGGGAAGGGGCGAGCTCATGTTAGGTTTCCAGGAGGGGCTACCTGTTGA  
CTGTCTTTGCAGGAAGAAGAAAACACCTGAGTGACCAGATGTCCCAGCTCCAGGTGCCTTGCC  
AGATGGCCAGAACCACACCTCTTGAAGAGTGACAGTGCTGTGGAGCATGGTTTCTGCACACCT  
GGAATGACTGGAACCCCAAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA  
ACAGAAGGCTGTGGACCACCTGTGAGATGGAGAAGTCCTTCTGAGGCTATCCAAACACGGAC  
CAGGCCATGAGACCCCGATGACCATCCCTGAATTTTTTTCGAGAGTCAGTCAACCGATTTGGAA  
CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAAGTGGGAAATTCTGAATTTCAACCAGTACT  
ATGAGGCTTGTGGAAGGCTGCAAAATCCTTGATCAAGCTGGGTTTGGAGCGTTTCCACGGAG  
TTGGTATCCTGGGGTTTAACTCTGCAGAGTGGTTTATCACTGCTGTTGGTGCCATCCTAGCCG  
GGGGTCTTTGTGTTGGTATTTATGCCACCAACTCTGCCGAGGCTTGTCAATATGTCATCACTC  
ATGCCAAAGTGAACATCTTGCTGGTTGAGAATGATCAACAGTTACAGAAAATCCTTTCGATTC  
CACAGAGCAGCCTAGAGCCCCATAAAGCGATCATCCAGTACAGACTGCCAATGAAGAAGAACA  
ACAACTTGTACTCTTGGGATGATTTTCATGGAACCTTGGCAGAAGTATCCCTGACACCCAACCTGG  
AGCAGGTCATCGAGAGCCAGAAGGCGAATCAATGCGCAGTGCTCATCTACACTTCAGGGACCA  
CAGGCATACCCAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGCAGGAGCAGTGA  
CAAAGGACTTTAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCCACTCAGCCATA  
TTGCAGCACAGATGATGGACATCTGGGTACCCATAAAGATTGGGGCGCTCACATACTTTGCTC  
AAGCAGATGCTCTCAAGGGCACCTTGGTAAGTACTCTAAAGGAGGTAAACCTACTGTCTTCA  
TTGGAGTGCCTCAAATTTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAGTCCA  
TGGGCTTGAAGAAGAAGGCATTTCGTGTGGGCAAGAAACATTGGCTTCAAGGTCAACTCAAAAA  
AGATGTTGGGGAAATATAATACTCCCGTGAGCTACCGCATGGCTAAGACTCTCGTGTTTCAGCA  
AAGTCAAGACATCCCTTGGCTTGGATCACTGTCACTCTTTTATCAGTGGGACTGCGCCCCCTCA  
ACCAAGAGACTGCCGAGTTCTTTCTAAGCTTGGACATACCTATAGGCGAGTTGTATGGGTTGA  
GTGAGAGCTCGGGACCCACACGATATCCAACCAGAATAACTACAGGCTTCTAAGCTGTGGCA  
AGATCTTGACTGGGTGTAAGAATATGCTGTTCCAGCAGAACAAGGATGGCATTGGGGAGATCT  
GCCTCTGGGGTAGGCACATCTTCATGGGCTATCTGGAAAAGTGAGACTGAACTACAGAGGCCA  
TCGATGATGAAGGCTGGCTACACTCTGGGGATCTGGGCCAGCTGGACGGTCTGGGTTTCTCTCT  
ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGGTGAAAATGTGCCCCCATTC  
CTGTTGAGACCTTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA  
AACTGAAGTTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCGGAGAAC  
CTCTGGACAAGCTGAACTTCGAGGCCATCAACTTCTGTCGGGGTCTGGGCAGCCAGGCATCCA  
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCCCTGGTCTACAAGGCCATCCAGCAAGGCATCA  
ATGCTGTGAACCAGGAAGCCATGAACAATGCACAGAGGATTGAAAAGTGGGTCTCTTGGAGA  
AGGACTTTTCCATCTATGGTGGAGAGCTAGGTCCAATGATGAACTTAAGAGACATTTTGTAG  
CCCAGAAATACAAAAAACAAATTGATCACATGTACCACCTGACTGCTTTGATGGAGCTGCTCTC  
AGCTGTTCTGATGCCTTCAGCAGGAAGACCTCATTGCAATAAGTGAAATGCTGCTCTAGGTAG  
AAGCTCTCCCTGCTGTTTTTAAGAAGCCACATTCCTCATTGGTCAGTTTCTTGATTGTTTCGTC  
TGTTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTTCAAAGCAATAAAATCACTGTATA  
TCTTTCTAAGGACCTTCAAGTCATGACTCCAGGGAAGCCTATTGGGAAGTCTACTAAAACTG  
CCTGATTTACAAGAAAGACCTGAACTTGTGGGCTCCCATTTGATTTTTTCTCCTCAGGGGAC  
TCAGACATTAGAAAGAAAAAGCCTCACAGATTTGAAGAACTGGACCCCCAAATCAACTCACCT  
GCCTGGAAGCAACTGGGAAACCTTCCAATAAGTCCTGATAATAAAGCACTTCAGGGTCCCAA  
AAAAAAAAA

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**FIGURE 206**

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAASLIKGLERFHGVGILGF  
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQQLQKILSIPQSSLE  
PLKAI IQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTSGTTGIPKG  
VMLSHDNITWIAGAVTKDFKLTDKHETVVSYLPLSHIAAQMMDIWVPIKIGALTYFAQADALK  
GTLVSTLKEVKPTVFIGVPQIWEKIHVMVKKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKY  
NTPVSYRMAKTLVFSKVKTSGLDLHCHSFISGTAPLNQETAEFFLSLDIPIGELYGLSESSGP  
HTISNQNNYRLSCGKILTGCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW  
LHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPIISNAMLVGDKLKFLS  
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQQDPLVYKAIQQGINAVNQE  
AMNNAQRIEKWVILEKDFSIYGGELGPMMLKRRHFVAQKYKKQIDHMYH

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 65-86

**N-glycosylation site.**

amino acids 196-200

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 282-286

**Tyrosine kinase phosphorylation sites.**

amino acids 547-555, 608-616

**N-myristoylation sites.**amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,  
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

**Putative AMP-binding domain signature.**

amino acids 177-189

**Putative AMP-binding domain proteins.**

amino acids 173-190



**FIGURE 207**

[illegible]

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**FIGURE 208**

MAYRVLGRAGPPQPRRARLLFAFTLSLSCTYLCYSFLCCDDLGRSRLLGAPRCLRGPSAGG  
QKLLQKSRPCDPSGPTPSEPSAPSAPAAVPAPRLSGSNHSGSPKLGTKRLPQALIVGVKKGG  
TRAVLEFIRVHPDVRLGTEPHFFDRNYGRGLDWYRSLMPRTLESQITLEKTPSYFVTQEAPR  
RIFNMSRDTKLIVVVRNPVTRAISDYTQTLSSKKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM  
YVLHLESWLQYFPLAQIHVSGERLITDPAGEMGRVQDFLGIKRFITDKHFYFNKTKGFPCLK  
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPYNIKFYETVGQDFRWE

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 102-106, 193-197, 235-239, 306-310

**Tyrosine kinase phosphorylation site.**

amino acids 296-305

**N-myristoylation sites.**

amino acids 51-57, 100-106, 121-127, 125-131

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 20-31

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**FIGURE 209**

CTTTCCTTATCTGTGTGTACTCTTATCTCACTGTTCTATTTTTCTCCTCATTTATATTAAC  
CTTTCCTTACCTTTTTTCTGAACCTTCTAGGCCTTCTCTTCCAGAACTGGTGGAAAGACAAATG  
AAACGGCCAAGATGGTAAGAAACAAGCCGCATTTCTCCTTGGGGAGACTGATAATTTAAAAGG  
TTTGTGTGTGTCAGAAACATTCCCAGCTTCATCACCACCCCTTTCCTTCCACCTCTGCCCCTG  
GAGACCACTTACATCCCGAAGCGGACGCGGCAGCTGAAGTCAGGAAACCATGCATCACATTAG  
CAGGAGCCAACTGCAGACTTTAACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGT  
CCAGACAAGCCGGGGCAGCTCATAAACTGGTTCATCTGCTCCCTGTGCGTCCCGCGGGTGCCT  
AAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAACCTTCTGCTGGGCACTGCGTGTGCC  
ATCTACTTGGGCTTCTTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACAGGCGGCT  
GAGAAGGGGCCACATCGCAGCCGCGACACCGCCGAGCCATCCTTCCCTGAGATACCCCTGGAT  
GGTACCCTGGCCCCCTCCAGAGTCCCAGGGCAATGGGTCCACTCTGCAGCCCAATGTGGTGTAC  
ATTACCCTACGCTCCAAGCGCAGCAAGCCGGCCAATATCCGTGGCACCGTGAAGCCCAAGCGC  
AGGAAAAGCATGCAGTGGCATCGGCTGCCCCAGGGCAGGAGGCTTTGGTTCGGACCATCCCTT  
CAGCCGCAGGAAGCGGCAAGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAAC  
CTGGTTAAGATTGGAGAGCGACCTGGAGGTTGGTGCGGGGTCCGGGAGTGCAGCCGGGGGC  
CCAGACTTCTTGACAGCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAGCGCCCC  
TCCTGGCTGAGCAAAGATGACATCCGAAGAATGCGACTCTTGGCGGACAGCGCAGTGGCAGGG  
CTCCGGCCTGTGTCTCTAGGAGCGGAGCCCGTTTGTGCTGGTGTGGAGGGGGGCGCACCTGGC  
GCTGTGCTCCGCTGTGGCCCTAGCCCCGTGTTGGCTTCTCAAGCAGCCCTTGGACATGAGTGAG  
GTGTTTGCCTTCCACCTAGACAGGATCCTGGGGCTCAACAGGACCCTGCCGTCTGTGAGCAGG  
AAAGCAGAGTTCATCAAGATGGCCGCCCATGCCCATCATTTCTTTGGGATGCATCTTTATCT  
TCAGCAAGTAATGACACCCATTCTTCTGTTAAGCTCACCTGGGGAACCTTATCAGCAGTTGCTG  
AAACAGAAATGCTGGCAGAAATGGCCGAGTACCAAGCCTGAATCAGGTTGTACTGAAATACAT  
CATCATGAGTGGTCCAAGATGGCACTCTTTGATTTTTTGTACAGATTTATAATCGCTTAGAT  
ACAAATTGCTGTGGATTTCAGACCTCGCAAGGAAGATGCCTGTGTACAGAAATGGATTGAGGCCA  
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGACCCAAGG  
CATTTGGTTTTTATAGACAACAAGGGTTTTCTTTGACAGGAGTGAAGATACTTAACTTCAA  
TTGTTAGAAGGCATCAAAGAGTTTCCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTA  
CGGCAGAACTTCTTCAGTCTCTGTTTCTTGATAAAGTGTATTGGGAAAGTCAAGGAGGTAGA  
CAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAAATTCTTATCACCTATATC  
AATGCACACGGGGTCAAAGTATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTG  
TTAGATATATTTATGCATTTTTGGTTTTGTTTTTAAATCAAGCACATCAACCTCAAGCCCGTT  
TAGCAATGAGGCAGTGTAGATGAATACGTAAAATAAATGACTTTAACCAAGTAGCTATAAAGG  
GACTTAGCACTGTATGCATACTTAAAAAGGTTTTGAAAAACAACTACTTGAGAAATATTTGT  
TTATATTTTTCTCTAACATCATGCTATGTGTGAGTCTGAACATCTGACAACAGAAATTTAGT  
TATTATTCTAGCTAAGTTTTGAAAAATTTGTGATGCTGTTTAAATAGAAAACCTGCAAACCAGA  
GATACTGACTCCATTAATAAACCATATTTTGTGCCGTTTTGACTGTTCTGACCAAATACTAAT  
GGGAACAATTCTTGACGTTTTTCTGTTGCTGATTGTTAACATAGAGCAGTCTCTACACTACCC  
TGAGGCAACTCTACATTGGAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGACCATA  
CATTTAAACAGAAATGCTGGTTTTATTTGCAAAATCACCAGTATATTTTCTATTGTGTCTATAA  
AAAATCAGTCATTTAAGTACAAGAATCATATTTTCCATTCTTTTTAGAAATTTATTTGTTG  
TCCCTATGGAAATCATTCACATCTGACAATTTATATGTTAAAGAGTTTTACTCTCTATTTT  
GGTCCAATTTGTATCTAGTGGCTGAGAAATTAATAATTCTAAAGTATGAAGTTACCTATCTG  
AAAATGTACTTACAGAGTATCATTTTAAATGGATGTCTCTTAAAAATTTTGTACTTTTAC  
CAACAATGTAATATAATTTATGTATATTTTATTAATAATAGTGAATTCCTTAAATTTGTTCT  
ATGTACTTATATTTAATTTGATTTAATGGTTACTGCCAGATATTGAGAAATGGTTCAAATAT  
TGAGTGTGTTTCAATAA

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**FIGURE 210**

MTC PDKPGQLINWFICSLCVPRVRKLWSSRRPRTTRNLLLGTACAIYLGFLVSQVGRASLQHG  
QAAEKGP HRSRDTAEPSFPEIPLDGT LAPPESQGN GSTLQPNVYITLRSKR SKPANIRGTVK  
PKRRKKH AVASAAPGQEALVGPSLQ PQEAAREADAVAPGYAQGANLVKIGERPWRLVRGPGVR  
AGGPDFLQ PSSRESNIRIYSESAPSWLSKDDIRRMRL LADSAVAGLRPVSSRSGARLLVLEGG  
APGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGLNRTLPSVSRKAEFIQDGRPCPIILWDA  
SLSSASNDTHSSVKLTWGT YQQLLKQKCWQNGRVPKPESGCTEIH HHEWSKMALFDLLQIYN  
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAA LAHI IQRKHDPRHLVFIDNKGFFDRSEDNL  
NFKLLEGIKEFPASAVSVLKSQH LRQKLLQSLFLDKVYWESQGG RQGIEKLIDVIEHRAKILI  
TYINAHGVKVLPMNE

**Transmembrane domain:**

amino acids 40-56

**N-glycosylation sites.**

amino acids 98-102, 289-293, 322-326

**N-myristoylation sites.**amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,  
287-293, 484-490

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**FIGURE 211**

GTGGGGTGGTGAGCGCAGCGCCGAGGATGAGGAGGTGCAACAGCGGCTCCGGGCCCGCCCGCTCGCTGCTGCTGC  
TGCTGCTGTGGCTGCTCGCGGTTCCCGGCGCTAACGCGGCCCCGCGGTGCGCGCTCTATTGCGCTTCCGACCCGC  
TGACGCTGCTGCAGGCGGACACGGTGCGCGGCGCGGTGCTGGGCTCCCGCAGCGCTGGGCCGTGGAGTTCTTCG  
CCTCCTGGTGCGGCCACTGCATCGCCTTCGCCCCGACGTGGAAGGCGCTGGCCGAAGACGTCAAAGCCTGGAGGC  
CGGCCCTGTATCTCGCCGCCCTGGACTGTGCTGAGGAGACCAACAGTGCAGTCTGCAGAGACTTCAACATCCCTG  
GCTTCCCGACTGTGAGGTTCTTCAAGGCCTTTACCAAGAACGGCTCGGGAGCAGTATTCCAGTGGCTGGTGCTG  
ACGTGCAGACGCTGCGGGAGAGGCTCATTGACGCCCTGGAGTCCCATCATGACACGTGGCCCCCAGCCTGTCCCC  
CACTGGAGCCTGCCAAGCTGGAGGAGATTGATGGATTCTTTGCGAGAAATAACGAAGAGTACCTGGCTCTGATCT  
TTGAAAAGGGAGGCTCTACCTGGGTAGAGAGGTGGCTCTGGACCTGTCCAGCACAAAGGCGTGGCGGTGCGCA  
GGGTGCTGAACACAGAGGCCAATGTGGTGAGAAAGTTGGTGTCACCGACTTCCCCCTCTTGCTACCTGCTGTTC  
GGAATGGCTCTGTCTCCCGAGTCCCCGTGCTCATGGAATCCAGGTCTTCTATACCGCTTACCTGCAGAGACTCT  
CTGGGCTCACCAGGAGGCTGCCCAGACCACAGTTGCACCAACCAGTGTACAAGATAGCTCCCAGCTGTTTGGGA  
AATTGGCAGATCGCTCCAAGATCTACATGGCTGACCTGGAATCTGCACTGCACACTACATCCTGCGGATAGAAGTGG  
GCAGGTTCCCGGTCTCGGAAGGGCAGCGCCTGGTGGCCCTGAAAAAGTTTGTGGCAGTGCTGGCCAAGTATTTCC  
CTGGCCGGCCCTTAGTCCAGAACTTCTGCACTCCGTGAATGAATGGCTCAAGAGGCAGAAGAGAAATAAAATTC  
CCTACAGTTTCTTTAAACTGCCCTGGACGACAGGAAGAGGGTGCCGTTCTTGCCAAGAAGGTGAACTGGATTG  
GCTGCCAGGGGAGTGAGCCGCATTTCCGGGGCTTCCCTGCTCCCTGTGGGTCTTCCACTTCTTGACTGTGC  
AGGCAGCTCGGCAAAATGTAGACCACTCACAGGAAGCAGCCAAGGCCAAGGAGGTCTCCAGCCATCCGAGGCT  
ACGTGCACTACTTCTTCGGCTGCCGAGACTGCGCTAGCCACTTCGAGCAGATGGCTGCTGCCTCCATGCACCGGG  
TGGGGAGTCCCAACGCCGCTGTCTCTGGCTCTGGTCTAGCCACAACAGGGTCAATGCTCGCCTTGCAAGGTGCC  
CCAGCGAGGACCCCCAGTTCCCCAAGGTGCAGTGGCCACCCCGTGAACCTTTGTTCTGCTGCCACAATGAACGCC  
TGGATGTGCCCGTGTGGGACGTGGAAGCCACCCTCAACTTCTCAAGGCCCACTTCTCCCCAAGCAACATCATCC  
TGGACTTCCCTGCAGCTGGGTGAGCTGCCCCGAGGGATGTGAGAATGTGGCAGCCGCCCCAGAGCTGGCGATGG  
GAGCCCTGGAGCTGGAAAGCCGGAATTCAACTCTGGACCTGGGAAGCCTGAGATGATGAAGTCCCCCACAACA  
CCACCCACATGTGCCGCTGAGGGACCTGAGGCAAGTCGACCCCGAAGCTGCACCTGGCCTCAGAGCTGCAC  
CAGGCCAGGAGCCTCCTGAGCACATGGCAGAGCTTCAGAGGAATGAGCAGGAGCAGCCGCTTGGGCAGTGGCACT  
TGAGCAAGCGAGACACAGGGGCTGCATTGCTGGCTGAGTCCAGGGCTGAGAAGAACCCTCTGGGGCCCTTTGG  
AGGTGAGGCGCGTGGGCCGAGCTCCAAGCAGCTGGTGCAGATCCCTGAGGGCCAGCTGGAGGCCCCGAGCTGGAC  
GGGGCCGAGGCACTGGCTGCAGGTGCTGGGAGGGGCTTCTCTTACCTGGACATCAGCCTCTGTGTGGGGCTCT  
ATTCCCTGTCTTCTCATGGGCTGCTGGCCATGTACACCTACTTCCAGGCCAAGATAAGGGCCCTGAAGGGCCATG  
CTGGCCACCCTGCAGCTGGAACCACTGGGGAGGAGGCGGGAGAGGGAGCTGCCATCTCTAGGCACCTCAAGCCC  
CCTGACCCCATTCCTCCCTCCCAACCCCTTGCTCCTTGCTGGCCTAGAAGTGTGGGAAATTGAGGAAAACGAG  
TTGCTCCAGTGAAGCTTCTTGGGGTTGCTAGGACAGAGAGCTCCTTTGACACAAAAGACAGGAGCAGGGTCCAGG  
TTCCCTGCTGTGCAAGGAGGGCAGCCCCGGGCAGTGGGCATAGGGCAGCTCAGTCCCTGGCCTCTTAGCACCAC  
ATTCTGTGTTTTTCACTTATTTGAAGTCTGCCTCATTCTCACTGGAGCCTCAGTCTCTCTGCTTGGTCTTGGC  
CCTCAACTGGGGCAAGTGAAGCCAGAGGAGGGTCCCCCAGCTGGGTGGGCTGGAATGGAACCTCTCACTAGCTGC  
TGGGGCTCCGCCACCCTGCTCCCTTCCGGACAATGAAGAAGCCTTTGCACCTGGGAGGAAGGACCACCCCGGG  
CCCTCTATGCCTGGCCAGCCTCCAGCTCCTCAGACCTCCTGGGTGGGGTTTGGCTTCAGGGTGGGGTTTGAAGC  
TTCTGGAAGTCGTGCTGGTCTCCAGGTGAGGCAAGCCATGGTTGCTGGGCTGTAGGGTGAGTGGCTTGGTGGT  
GGGACCTGACGAGTTGGTGGCATGGGAAGGATGTGGGTCTCTAGTGCCTTGCCCTGGCTTAGCTGCAGGAGAAGA  
TGGCTGCTTTCACTTCCCCCATTTAGCTCTGCTCCTCTGAGCCTGGTCTTTTGTCTTTTTTATTTTGGTCTC  
CAAGATGAATGCTCATCTTTGGAGGGTGCCAGGTAGAAGCTAGGGAGGGGAGTGTCTTCTCTCCTCAGGTTTAC  
CTTCCAGTGTGAGAAGTTAGAAGGGTCTGGCGGGGCGAGTGCCTTACACATGCTTGATTCCCACGCTACCCCT  
GCCTTGGGAGGTGTGTGAATAAATTATTTTTGTTAAGGCA

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**FIGURE 212**

MRRCSGSGPPPSLLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAWAV  
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDFNIPGFPTVRFFKA  
FTKNGSGAVFPVAGADVQTLRERLIDALESHHDTWPPACPPLEPAKLEEIDGFFARNNEEYLA  
LIFEKGGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFFPSCYLLFRNGSVSRVPVL  
MESRSFYTAYLQRLSGLTREAAQTTVAPTTANKIAPTVMKLADRSKIYMADLESALHYILRIE  
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDR  
KEGAVLAKKVNWIGCQGSEPHFRGFPCSLWVLFHFLTVMQARQNVDSQEAAKAKEVLPAIRG  
YVHYFFGCRDCASHFEQMAAASMRVGSFNAAVLWLWSSSHNRVNARLAGAPSEDPQFPKVQWP  
PRELCSACHNERLDVPVWDVEATLNFLKAHFSPSNIILDFPAAGSAARRDVQNVAAPPELAMG  
ALELESRNSTLDPGKPEMMKSPTNTTPHVPAGEPEASRPPKLHPGLRAAPGQEPPEHMAELQR  
NEQEQLGQWHLKRDGTGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGRG  
RGQWLQVLGGGFSYLDISLCVGLYSLSFMGLLAMTYTFQAKIRALKGHAGHPAA

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 705-728

**N-glycosylation sites.**

amino acids 130-134, 243-247, 575-579

**Glycosaminoglycan attachment site.**

amino acids 6-10

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 644-648

**N-myristoylation sites.**amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,  
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

**Thioredoxin family proteins**

amino acids 62-78

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**FIGURE 213**

GCACGAGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACAC  
TGAGATCATCCGGCTCAAGGAGCAAGGTTCCGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGA  
GTCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCT  
TATGGCAACCATCGTGCGTCTCTGCTGTGCCCCGTCCAGAGAAATCTCAAAGGTGTTGTGTC  
AGCCAAAATGATATCCGAGTGGAATTGTCCACAAGGAACCAGCCTCTGGTCGGGAGGGTGA  
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGGTGAATTCCAGCAAGACTCAGTCCT  
GAAACAGCTGGAGGTCCTCAAAGAAGAGGAGAAAGAGTTTCAGAACCTGAAGGACCCACCAA  
TGGCTACTACAGCGTCAACACCTTCAAAGAGCACCCTCAACCCCGACCATCTCCCTCTCCAG  
CTGCCAGCCCGACCTGCGTCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCTTACACAA  
CATCTACAGCACCTGAGCGGCCAGGGCCGCTCTACGACTACGGGCAGCGGTTTGTGCTGGG  
CATGGGCAGCTCGTCCATCGAGCTTTGTGAGCGGGAGTTCCAGAGAGGCTCCCTCAGCGACAG  
CAGCTCCTTCCTGGACACGCAGTGTGACAGCAGCGTCAGCAGCAGCGGCAAGCAGGATGGCTA  
TGTGCAGTTCGACAAGGCCAGCAAGGCTTCTGCTTCCTCCTCCCACCACTCCCAGTCCTCGTC  
CCAGAACTCTGACCCCAGTCGACCCCTGCAGCGGCGGATGCAGACTCACGTCTTAAGGATCACA  
CACCGCGGGTGGGGACGGGCCAGGGAAGAGGTCAGGGCACGTTCTGGTTGTCCAGGGACGAGG  
GGTACTTTGCAGAGGACACCAGAATTGGCCACTTCCAGGACAGCCTCCAGCGCCTCTGCCAC  
TGCCTTCCTTCGAAGCTCTGATCAAGCACAAATCTGGGTCCCCAGGTGCTGTGTGCCAGAGGT  
GGGCGGGTGGGGAGACAGACAGAGGCTGCGGCTGAGTGCGCTGTGCTTAGTGCTGGACACCCG  
TGTCCCCGGCCCTTTCTGGAGGCCCTCTACCACCTGCTCTGCCACAGGCACAAGTGGCAG  
CTATAACTCTGCTTTCATGAACTGCGGTCCACTCTCTGGTCTCTCTGTGGGCTCTACCCCTC  
ACTGACCACAAGCTCTACCTACCCCTGTGCCTGTGCTCCCATAACAGCCCTGGGGAGAAGGGGA  
TGACGTCTTCCCAGCACTGAGCTGCCCCAGAAACCCCGGCTCCCCACTGCTGCTCATAGCCCA  
TACCCTGGAGGCTGACAAGCCAGAAATGGCCTTGGCTAAAGGAGCCTCTCTCTCACCAGGCTG  
GCCGGGAGCCCACCCCAATTTGTTTGGTGTTTTGTGTCCATACTCTTGAGTTCTGTCTTG  
GACTTGATGCCGCTGAACTCTGCGGTGGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGA  
GGGAGGGAGGAGGGAGCCTGTGCTGACGGAGCACCTCGCCGGGTGTGCCCCCTCCTGGGCTGTG  
TGACCCAGCCTCCCCACCCACCTCCTGCTTTGTGTACTCCTCCCCTCCCCCTCAGCACAATC  
GGAGTTCATATAAGAAGTGCGGGAGCTTCTCTGGTCAGGGTTCTCTGAACACTTATGGAGAGA  
GTGCTTCCTGGGAAGTGTGGCGTTTGAAGGGGCTGGAGGGCAGGTCTTTAAGATGGCGAGACT  
GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTTCAGTAAGGCTCCACGAGAAGA  
GAGGAAGTATATCTACACCTCAACCCTCCTAGTCACCACCTGAAATAAATGTTAGGGAAAAAAA

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**FIGURE 214**

MAVIIGVAVGAGVAFLVLMATIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHS  
TIKQLMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCQP  
DLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSSF  
LDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 150-154

**N-myristoylation sites.**

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 114-125



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**FIGURE 215**

CAGCCTTCCTCCCCAGCCTGAGTGACTACTCTATTCCCTTGGTCCCTGCTATTGTCGGGGACG  
ATTGCA**ATG**GGCTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGGCTGGCG  
CCTGCTATTGCATTTATAGACTGACTAGGGGAAGAAAACAGAACAAGGAAAAAATGGCTGAGG  
GTGGATCTGGGGATGTGGATGATGCTGGGGACTGTTCTGGGGCCAGGTATAATGACTGGTCTG  
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGGCTCGGATTG  
GGACTGAAGCTGGAACCAGAGCTAGGGCCAGGGCAAGGGCCAGGGCTACCCGGGCACGTCGGG  
CTGTCCAGAAACGGGCTTCCCCCAATTCAGATGATACCGTTTTGTCCCCTCAAGAGCTACAAA  
AGGTTCTTTGCTTGGTTGAGATGTCTGAAAAGCCTTATATTCTTGAAGCAGCTTTAATTGCTC  
TGGGTAACAATGCTGCTTATGCATTTAACAGAGATATTATTCGTGATCTGGGTGGTCTCCCAA  
TTGTCGCAAAGATTCTCAATACTCGGGATCCCATAGTTAAGGAAAAGGCTTTAATTGTCCTGA  
ATAACTTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTGTG  
ATGACACAATCACTTCTCGCTTGAACCTCATCTGTGCAGCTTGCTGGACTGAGATTGCTTACAA  
ATATGACTGTTACTAATGAGTATCAGCACATGCTTGCTAATTCCATTTCTGACTTTTTTTCGTT  
TATTTTCAGCGGGAAATGAAGAAACCAAACCTTCAGGTTCTGAAACTCCTTTTGAATTTGGCTG  
AAAATCCAGCCATGACTAGGGAACCTGCTCAGGGCCCAAGTACCATCTTCACTGGGCTCCCTCT  
TTAATAAGAAGGAGAACAAAGAAGTTATTCTTAAACTTCTGGTCATATTTGAGAACATAAATG  
ATAATTTCAAATGGGAAGAAAATGAACCTACTCAGAATCAATTCGGTGAAGGTTCACTTTTTT  
TCTTTTTTAAAAGAATTTCAAGTGTGTGCTGATAAGGTTCTGGGAATAGAAAGTCACCATGATT  
TTTTGGTGAAAGTAAAAGTTGGAAAATTCATGGCCAAACTTGCTGAACATATGTTCCCAAAGA  
GCCAGGAAT**TAA**CACCTTGATTTTGTAAATTTAGAAGCAACACACATTGTAAACTATTCATTTTC  
TCCACCTTGTTTATATGGTAAAGGAATCCTTTCAGCTGCCAGTTTTGAATAATGAATATCATA  
TTGTATCATCAATGCTGATATTTAACTGAGTTGGTCTTTAGGTTTAAGATGGATAAATGAATA  
TCACTACTTGTTCTGAAAACATGTTTGTTGCTTTTTATCTCGCTGCCTAGATTGAAATATTTT  
GCTATTTCTTCTGCATAAGTGACAGTGAACCAATTCATCATGAGTAAGCTCCCTTCTGTCATT  
TTCATTGATTTAATTTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

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**FIGURE 216**

MGYARKVGVVTAGLVIGAGACYCIYRLTRGRKQNKEKMAEGGSGDVDDAGDCSGARYNDWSDD  
DDDSNESKSIVWYPPWARIGTEAGTRARARARARATARRAVQKRASPNSDDTVLSPQELQKV  
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKALIVLNN  
LSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFRRLF  
SAGNEETKLQVLKLLLNLAE NPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN  
FKWEENEPTQNQFGEGLFFFLKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 68-72, 189-193, 217-221, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-111

**N-myristoylation sites.**amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,  
290-296**Amidation site.**

amino acids 29-33

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FIGURE 217

[illegible]

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**FIGURE 218**

MAIAQLATEYVFSDFLKEPTEPKFKGLRLELAVDKMVTCTIAVGLPLLLISLAFQEISIGTQ  
ISCFSPPSSFSWRQAAFVDSYCWAAVQQKNSLQSESGNLPLWLHKFFPYILLFFAILLYLPPLF  
WRFAAAPHICSDLKFIMEELDKVYNRAIKAAKSARDLDMRDGACSVPGVTENLGQSLWEVSES  
HFKYPIVEQYLKTKKNSNNLI IKYISCRLLTLIIILLACIYLGYYFSLSSLSDEFVCSIKSGI  
LRNDSTVPDQFQCKLIAVGIFQLLSVINLVVYVLLAPVVVYTLFVPPRQKTDVLKVYEILPTF  
DVLHFKSEGYNDLSLYNLFLEENISEVKSYSKCLKVLENIKSSGQGIDPMLLLTNLGMKMDVV  
DGKTPMSAEMREEQGNQTAELQGMNIDSETKANNGEKNARQRLDSSC

**Transmembrane domains:**

amino acids 37-55, 108-126, 216-232, 273-290

**N-glycosylation sites.**

amino acids 255-259, 338-342, 394-398

**Glycosaminoglycan attachment site.**

amino acids 357-361

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 61-67, 174-180, 251-257, 393-399

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 218-229

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**FIGURE 219**

CTGTGAGTGACACACGCTGAGTGGGGTGAAGGGAAATGCTGGTGAATTTCAATTTGAGGTGTG  
GGTTGCTGTTAGTCACTCTGTCTCTTGCCATTGCCAAGCACAAAGCAATCTTCCTTCACCAAAA  
GTTGTTACCCAAGGGGAACATTGTCCCAAGCTGTTGACGCTCTCTATATCAAAGCAGCATGGC  
TCAAAGCAACGATTCCAGAAGACCGCATAAAAAATATACGATTATTAAAAAAGAAAACAAAA  
AGCAGTTTATGAAAACTGTCAATTTCAAGAACAGCTTCTGTCCTTCTTCATGGAAGACGTTT  
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTTGTGGAGGACTTTCATAGCCTTA  
GGCAGAAATTGAGCCACTGTATTTCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA  
GGATGAAAAGAATATTTTATAGGATTGGAACAAAGGAATCTACAAAGCCATCAGTGAAGTGG  
ATATTCTTCTTTCCTGGATTAAAAAATTATTGGAAAGCAGTCAGTAAACCAAAGCCAAGTACA  
TTGATTTTACAGTTATTTTGAAATACAATAAGAACTGCTAGAAATATGTTTATAACAGTCTAT  
TTCTTTTAAAACTTTTAAACATAATACTGACGGCATGTTAGGTGATTCAGAATAGACAAGAA  
GGATTTAGTAAATTAACGTTTTGGATATAAGTTGTCACATAATTTGCACATTTTCTGTGTTTTC  
AAATAATGTTTCCATTCTGAACATGTTTTGTCATTCACAAGTACATTGTGTCAACTTAATTTA  
AAGTATGTAACCTGAATTAACCTCGTGTAAATATTTGTGTGTGGAGTGGGATGTGGGGGGTGGAG  
GGGGAATGACAGATTTCTGGAATGCAATGTAATGTTACTGAGACTTAAATAGATGTTATGTAT  
ATGATTGTCTGTTTAAAGTGTGTTGAAAATTGTTAATTATGCCCAGTGTGAACTTAGTACTTAAC  
ACATTTTGATTTTAAATTAAATAAATTGGGTTTCCTTCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAA

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**FIGURE 220**

MLVNFILRCGLLLVTLSLAIAKHKQSSFTKSCYPRGTL SQAVDALYIKAAWLKATIPEDRIKN  
IRLLKKKTKKQFMKNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSLRQKLSHCISCAS  
SAREMKSITRMKRIFYRIGNKGIYKAISELDILLSWIKKLLESSQ

**Signal sequence:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 148-153

**Interleukin-10 proteins.**

amino acids 58-94, 74-102, 128-170

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**FIGURE 221**

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGACATGAGGCGGCCGGCGGGCGGTGCCGCTCC  
TGCTGCTGCTGTGTTTTGGGTCTCAGAGGGCCAAGGCAGCAACAGCCTGTGGTCGCCCCAGGA  
TGCTGAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCA  
TCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCCTGACGG  
CTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCCTGCTGGGGGCAAGGC  
AGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCCGGGTGAGGCAGGTGGAGAGCAACCCCC  
TGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCCT  
TCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGA  
ACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGAAGACCTCCTGCCCCGAACCGCGGATCC  
TGCAGAAACTCGCTGTGCCCATCATCGACACACCCAAGTGCAACCTGCTCTACAGCAAAGACA  
CCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGG  
GCAAGAAGGATGCCTGCAAGGGCGACTCGGGCGGCCCCCTGGTGTGCCTCGTGGGTCAGTCGT  
GGCTGCAGGCGGGGGTGATCAGCTGGGGTGAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCT  
ACATCCGTGTCACCGCCCACCACAACCTGGATCCATCGGATCATCCCCAACTGCAGTTCCAGC  
CAGCGAGGTTGGGCGGCCAGAAGTGAGACCCCCGGGGCCAGGAGCCCCCTTGAGCAGAGCTCTG  
CACCAGCCTGCCCCGCCACACCATCCTGCTGGTCCCTCCCAGCGCTGCTGTTGCACCTGTGAG  
CCCCACCAGACTCATTTGTAAATAGCGCTCCTTCCTCCCCTCTCAAATACCCTTATTTATTT  
ATGTTTCTCCCAATAAAAACCCAGCCTGTGTGCCAGCTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 222**

MRRPAAVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGS  
LIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA  
LVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTP  
KCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGES  
CARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGGQK

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 55-58, 79-82

**Casein kinase II phosphorylation sites.**

amino acids 121-124, 165-168, 167-170, 248-251

**Tyrosine kinase phosphorylation sites.**

amino acids 78-86, 197-203

**N-myristoylation sites.**

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

**Amidation site.**

amino acids 219-222

**Serine proteases, trypsin family, histidine active site.**

amino acids 71-76



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**FIGURE 223**

CAAG**ATG**TGGACAGCTCTTGTGCTCATTTGGATTTTCTCCTTGTCTTATCTGAAAGCCATGC  
GGCATCCAACGATCCACGCAACTTTGTCCCTAACAAAATGTGGAAGGGATTAGTCAAGAGGAA  
TGCATCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGCAGCTTCTCC  
TGTACATTGACCAAAGGGACTTCGGCAGCCCACCTCAACTCTATGGAAGTCACAACAGAGGA  
CACAAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC  
CATTGCTCCCACGGCTGTGGCCTCCAGTACGACTGCGGCCTCCATTACGACTGCGGCCTCCAG  
TATGACTGTGGCCTCCAGTGCTCCCACGACTGCAGCCTCCAGTACAACTGTGGCCTCCATTGC  
TCCCACGACTGCAGCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCCTCCC  
CGCGCCACGTCCACTTCCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCTCT  
CAGCACAGCCCTCGCACAAAGTGCCAAAGAGCAGCGCGTTGCCAAGAACAGCAACCCTGGCCAC  
ATTGGCCACACGTGCTCAGACTGTAGCGACCACAGCAAACACAAGCAGCCCCATGAGCACTCG  
TCCAAGTCCTTCCAAGCACATGCCCAGTGACACCGCGGCAAGCCCTGTACCCCCTATGCGTCC  
CCAAGCACAAAGGTCCCATTAGCCAGGTGTCAGTGGACCAGCCTGTGGTTAACACAACAAATAA  
ATCCACACCCATGCCCTCAAACACAACCCCAGAGCCCCGCCCCACCCCCACAGTGGTGACCAC  
CACCAAGGCACAAGCCAGGGAGCCAACTGCCAGCCCAGTGCCAGTACCTCACACCAGCCCAAT  
CCCTGAGATGGAGGCCATGTCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC  
CGCTGGGCCAGGCACATCCCAGGCACCGGAGCAGGTAGAGACTGAAGCCACACCAGGTACTGA  
TTCCACTGGGCCAACACCCAGGAGCTCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCCA  
GCCCAGCACCCAAGGCCAGTACATGGTGGTCACTACTGAGCCCCTCACCCAGGCCGTGGTAGA  
CAAACTCTCCTTCTGGTGGTGTGTTACTCGGGGTGACCCTTTTTCATCACAGTCTTGGTTTT  
GTTTGGCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCCAGGTGGACTACTTAAT  
CAACGGGATGTATGCGGACTCAGAAATG**TGA**AGGGGGGCGGGGGCCTGGCGGGAGGCCTGGCCC  
CTTCCTCGTCCTTTTCCTTTTGCCCTTGAGACCAAACCAAGTGCTTCCAAATTCTTTTGGTGCA  
ATTGAGGAGATATGCCAGATGCTTAAACACATTTAATTGCTGTCAGATTAATTCCATGATCAC  
TAAAGAGTTGCTGCTTTTTTTCATATTTATTTTTGTAAATGATTCTGTGCCAGGAGCAGCTGG  
GGTTCCACCTCAGGGTGGGGCGGGCAGGACCCCGTCTCCCCAGGTGTCGGAGCCTGACCTGA  
ATTAAAGTACTGACTGCTCGCCA

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**FIGURE 224**

MWTALVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDVTMAAASPV  
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM  
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPSL  
TALAQVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRPSPSKHMPSDTAASPVPMPRPQ  
AQGPISQVSVDQPVVNTTNKSTPMPSNTTPEPAPTPTVVTTTKAQAREPTASFPVPHTSPIP  
EMEAMSPTTQPSMPYTTQRAAGPGTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQP  
STQGQYMVVTTEPLTQAVVDKTLVLLVLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLIN  
GMYADSEM

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 396-420

**N-glycosylation sites.**

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

**Casein kinase II phosphorylation sites.**

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

**N-myristoylation sites.**

amino acids 68-73, 354-359

**Aldo/keto reductase family putative active site signature.**

amino acids 195-210

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**FIGURE 225**

GGAAGGCGCTCAAGGTGCGCGGCCCGGGGCGCGCTACTGGGGGCGCCCTCCGCGGTGGGCAGC  
GCGCCAGGGATCGGCCTGGGCAGCCGCGGGGCGCGCGAAGGCTGCGCTTTCCTACGGCCCCC  
CTCGCTTCCTCCGGCACGGCGGCAACGGAGATTTCTCTCGGGGAACTACGCGGATCCTTTT  
CGGGGATCCTCGCCCCGCCCCAGTTCTCCGCCCCCTCCCCTTTGCTGGGGCGCCTGGGCTGGC  
CCGCGCAGGGGAGGAGGCTCTGGCAGCCTGGGCAGGGAGGCGGCGGGGGGCGCGGAGCCGCT  
GGCCATCGATTCTCCCCGCCATGTGACGCCGTCCTTAGCCCTGCGACCCCCAGCGCGTCCCGG  
GCCTGCGCCTCCGCCCCGCGCGCAGCGCACGGATGCTTCTGCCGGGACGCGCACGCCAACC GC  
CGACGCCCCAGCCCGTGACGATCCCGGCCTCCGCCGGCAGGTAGAGCCGCCGGGGCAGCTCC  
TGCGCCTCTTCTACTGCACTGTCCTGGTCTGCTCCAAAGAGATCTCAGCGCTCACCGACTTCT  
CTGGTTACCTAACCAAACCTCTGCAAAACCACACCACCTATGCCTGTGATGGGGACTATTTGA  
ATCTACAGTGCCCTCGGCATTCTACGATAAGTGTCCAATCGGCATTTTATGGGCAAGATTACC  
AAATGTGTAGTTCCCGAGAAGCCTGCCTCCCAGAGGGAAGACAGCTTAACCTGTGTGGCAGCCA  
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACCAGCGGGCCTGCCACCTCCTGGTCAATA  
GCCGTGTTTTTTGGACCTGACCTTTGTCCAGGAAGCAGTAAATACCTCCTGGTCTCCTTTAAAT  
GCCAACCTAATGAATTAAAAAACAAACCGTGTGTGAAGACCAGGAGCTGAAACTGCACTGCC  
ATGAATCCAAGTTCTCAACATCTACTCTGCGACCTACGGCAGGAGGACCCAGGAAAGGGACA  
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCTTTTCGATTGCTTGCTTACTCAGCTTTGCAAG  
TCCTATCCCGAAGGTGCTATGGGAAGCAGAGATGCAAAATCATCGTCAACAATCACCATTTTG  
GAAGCCCCCTGTTTGCCAGGCGTGAAAAAATACCTCACTGTGACCTACGCATGTGTTCCCAAGA  
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAACCTTCTTTGAAGCAGAAAGATG  
GTGAATATGGTATAAACTTCGACCCAAGCGGATCGAAGGTTCTGAGGAAAGATGGAATTCTTG  
TTAGCAACTCTCTGGCAGCCTTTGCTTACATTAGAGCCCACCCAGAGAGAGCTGCCCTGCTGT  
TCGTGTCCAGTGTCTGCATCGGCCTGGCCCTCACACTGTGCGCCCTGGTCATCAGAGAGTCCT  
GTGCCAAGGACTTCCGCGACTTGACGCTGGGGAGGGAGCAGCTGGTGCCAGGAAGTGACAAGG  
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTCTGAGTCTGATTTCCAGGGG  
AACTGTGCGGGTTCTGTAGGACTTCATATCCTATATACAGTTCCATAGAAGCTGCAGAGCTCG  
CAGAAAGGATTGAGCGCAGGGAGCAAATCATTCAGGAAATATGGATGAACAGTGGTTTGGACA  
CCTCGCTCCCAAGAAACATGGGCCAGTTCTACTTGAAAACCACATGCATCTTGATGCGATCGCA  
CTTTCTGAAGAAGGAAGGATCCCAAATGCCCCCTCCAGTTCTGGTTACCTGTACCTTCTATGA  
AGGAGAATTCGTATGTCATTCAACACTCGTGAGGCCAGGAAGCTATTAAAGGGATGTTTCAA  
GCTGTTTCTAGCACATTCCAAAATAAATGAGGAGGGAGGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 226**

MLLPGRARQPPTPQPVQHPLRRQVEPPGQLRLFYCTVLVCSKEISALTDGSGYLTKLLQNH  
TTYACDGDYLNLCQPRHSTISVQSAFYGQDYQMCSSQKQASQREDSLTCVAATTFQKVLDECQ  
NQRACHLLVNSRVFGPDLCPGSSKYLLVSFKCQPNELKNKTVCEDQELKLHCHESKFLNIYSA  
TYGRRTQERDICSSKAERLPPFDCLSYSALQVLSRRCYGKQRCKIIVNNHHFGSPCLPGVKKY  
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEYGINFDPGSKVLRKDGILVSNLSLAAFAYI  
RAHPERAALLFVSSVCIGLALTLCALVIRESCAKDFRDLQLGREQLVPGSDKVEEDSEDEEEE  
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIWMNSGLDTS�PRNMGQFY

**Transmembrane domains:**

amino acids 32-49, 322-343

**N-glycosylation sites.**

amino acids 62-66, 165-169

**Tyrosine kinase phosphorylation site.**

amino acids 280-287

**N-myristoylation site.**

amino acids 302-308, 333-339, 428-434

**Amidation site.**

amino acids 191-195

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**FIGURE 227**

GGCACGAGGTGGAAGGGCTTTTACAAACAGATTGCTGGCCCCACCCCCAGAATTTCTCATCA  
GGAGTGGGCAAGACCAATCATTTGCATTTCTGACAAGTTCCCAGGAGCTGCAGCTGCTGGCCC  
TGGAACCACACTTTGAGAACCACTGCTTTAGACCAAACACCAAAGGAAGATGCAGCCACCCTC  
CTTTACATGTCACAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG  
CAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGGCTAGGAGTGAAGCGTGTCAACCATGG  
TCAGCTCATGGCCAGCCAGGAAAGCCTCTCTGCTGTGCGTCTGTGCAGTTCTTGTTCTTCCCT  
GGAGGACTCTTGATCGCCTGTGATCTTGGCCAGGAGACCAGGTGCCTGGGTCCCTTCCTGGA  
AGGGGACAAGTTACACACCCCAGCCCCATTTTCCCACCAACTTCTACATGCCTTGGGAGAACC  
TTCTACATGTTGGCTGCCCCCTTCCCCTATTTTCAGCAGTGCCCAGTCCTGCTTATAAACCTGA  
GGCCTGCTCCCCATACCTTCCCTGTGCAAGTGCCAGCCGTTATTCCAGGCAGCCCAATGTTGT  
TGAGGCCAGATGGATTCCCTGGAAGCAGCTGGCCCATGGATGTGAGTCATCACAGTATTCTAGA  
AACAGAGAAGAGGTCTTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAAACATACCCCT  
GTCCTTAGCTGATCTAGGTGGAAGCCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAA  
AGGAATTGTATCTAGGACTAA

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## **FIGURE 228**

MVSSWPARKASLLCVC AVLVL PWRTL GSPVILARRPGAWVPSWKGTSYTPQPHFPTNFYMPWE  
NLLHVGCP LPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLEAAGPWM

**Signal peptide:**

amino acids 1-27

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 8-12

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**FIGURE 229**

GGGAAGGGATGCAAGGAAGCCCTCCGGCGCTGCGCTCCGAGGCGGGAGACAGCGTCCCGCTGA  
AAATGTGTGTCTGACATGCAAGCTCAGTGGGGCAGAGACCCGTGGATTGCTGTGCCCTGCCCT  
CCGGACCTGGATCATGAAGGTGTTGGGAAGAAGCTTCTTCTGGGTGCTGTTTCCCGTCCTTCC  
CTGGGCGGTGCAGGCTGTGGAGCACGAGGAGGTGGCGCAGCGTGTGATCAAACGCACCGCGG  
GCGAGGGGTGGCTGCCATGCAGAGCCGGCAGTGGGTCCGGGACAGCTGCAGGAAGCTCTCAGG  
GCTTCTCCGCCAGAAGAATGCAGTTCTGAACAAACTGAAAACGCAATTGGAGCAGTGGAGAA  
AGACGTGGGCCTGTGCGATGAAGAGAAACTGTTTCAGGTGCACACGTTTGAAATTTTCCAGAA  
AGAGCTGAATGAAAGTGAAAATTCCGTTTTTCCAAGCTGTCTACGGACTGCAGAGAGCCCTGCA  
GGGGGATTACAAAGATGTCGTGAACATGAAGGAGAGCAGCCGGCAGCGCCTGGAGGCCCTGAG  
AGAGGCTGCAATAAAGGAAGAAACAGAATATATGGAACCTTCTGGCAGCAGAAAAACATCAAGT  
TGAAGCCCTTAAAAATATGCAACATCAAACCAAAGTTTATCCATGCTTGACGAGATTCTTGA  
AGATGTAAGAAAGGCAGCGGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTTTGACGACAA  
TAAATCAGTCAAGGGGGTCAATTTTGAGGCAGTTCTGAGGGTGGAGGAAGAAGAGGCCAATTC  
TAAGCAAAATATAACAAAACGAGAAGTGGAGGATGACTTGGGTCTTAGCATGCTGATTGACTC  
CCAGAACAACCAGTATATTTTGACCAAGCCAGAGATTCAACCATCCCACGTGCAGATCACCA  
CTTTATAAAGGACATTGTTACCATAGGAATGCTGTCCTTGCCTTGTGGCTGGCTATGTACAGC  
CATAGGATTGCCTACAATGTTTGGTTATATTATTTGTGGTGTACTTCTGGGACCTTCAGGACT  
AAATAGTATTAAGTCTATTGTGCAAGTGGAGACATTAGGAGAATTTGGGGTGTTTTTTACTCT  
TTTTCTTGTGGCTTAGAATTTTCTCCAGAAAAGCTAAGAAAGGTGTGGAAGATTTCCCTTACA  
AGGGCCGTGTTACATGACACTGTTAATGATTGCATTTGGCTTGCTGTGGGGGCATCTCTTGCG  
GATCAAACCCACGCAGAGCGTCTTCATTTCCACGTGTCTGTCCTTGTCAGCACACCCCTCGT  
GTCCAGGTTCCCTCATGGGCAGTGCTCGGGGTGACAAAGAAGGCGACATTGACTACAGCACCGT  
GCTCCTCGGCATGCTGGTGACGCAGGACGTGCAGCTCGGGCTCTTCATGGCCGTGATGCCGAC  
TCTCATACAGGCGGGCGCCAGTGCATCTTCTAGCATTGTCTGGAAGTTCTCCGAATCCTGGT  
TTTGATTGGTCAGATTCTTTTTTCACTAGCGGCGGTTTTTCTTTTATGTCTTGTATAAAGAA  
GTATCTCATTGGACCTATTATCGGAAGCTGCACATGGAAAGCAAGGGGAACAAAGAAATCCT  
GATCTTGGGAATATCTGCCTTTATCTTCTTAATGTTAACGGTCACGGAGCTGCTGGACGTCTC  
CATGGAGCTGGGCTGTTTCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGTGGTCACCGA  
GGAGATCGCCACCTCCATCGAACCCATCCGCGACTTCCTGGCCATCGTTTTCTTCGCCTCCAT  
AGGGCTCCACGTGTTCCCCACGTTTGTGGCGTACGAGCTCACGGTGCTGGTGTTCCTCACCTT  
GTCAGTGGTGGTGATGAAGTTTCTCCTGGCGGCGCTGGTCTGTCTCTCATTCTGCCGAGGAG  
CAGCCAGTACATCAAGTGGATCGTCTCTGCGGGGCTTGCCCAGGTCAGCGAGTTTTCTTTGT  
CCTGGGGAGCCGGGCGCGAAGAGCGGGCGTCACTCTCGGGAGGTGTACCTCCTTATACTGAG  
TGTGACCACGCTCAGCCTCTTGCTCGCCCCGGTGCTGTGGAGAGCTGCAATCACGAGGTGTGT  
GCCCAGACCGGAGAGACGGTCCAGCCTCTGATGGCTCGGAGATGATGGACCGTGGAAAGGAAG  
CGTCTGTGGGGAGTGAGCGCTTAGATGGCCAGCAGCTGCTCCTTCTGGGAAGCTCGCACCTTG  
GCAACAGAACAGCCCTCTAGCAGAGCGTCAGTGCAGTCGTGTTATCCCGGCTTTTACAGAATA  
TTCTTGTCCTATTTTAGAATTTTCCGGAGTAGTTTATTTGCAGTCTGTTGATTATGTGCAGTA  
GACCCGGGACACTGCGTTTTTACCGATCACCTTGAATGTGGTGCCTGGATGTGCCTTTTTTTTT  
TTTCCCTGAAATTATTATTAATTTTCTATTGTGAGTTCATCAGTTCATAGTTTTTTTTAGTAAA  
GAAGCAAAATTAAGGCTTTTAAAAATGTACAACCTTCAGAATTATAATCTGTTAGTCAAATA  
TTTGTTATTAAACATTTCTGTAATATGAAGTTGTAATCCTGGCCGTGAGCTTGGAAGCTTACT  
TTTGATTCTTAAAGCCTATGTTTTCTAAAATGAGACAAATACGGATGTCTATTTGCCTTTTAT  
TGTAACCTTTTAAATGAAATAATTTTCATGTCAATTTCTATTAGATATATCACTTAAATATTTG  
GTTTTAAATCACAAGAATATGTATTTCTTAATAAAGATAATTTATGATCATGGTAAAAAAAAA

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**FIGURE 230**

MKVLGRSFFWVLPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQWVRDSCRKLSGLLRQ  
KNAVLNKLKTAIGAVEKDVGLSDEEKLFQVHTFEIFQKELNESENSVFQAVYGLQRALQG DYK  
DVVNMKESSRQRLEALREAAIKEET EYMELLAAEKHQVEALKNMQHQNQSLSMLDEILEDVRK  
AADRLEEEIEEHAFDDNKS VKGVNFEAVLRVEEEEANSKQNITKREVEDDLGLSMLIDSQNNQ  
YILTKPRDSTIPRADHHFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPGSLNSIK  
SIVQVETLGEFGVFFTLFLVGLFESPEKLRKVWKISLQGPCYMTLLMIAFGLLWGHLRLRIKPT  
QSVFISTCLSLSSTPLVSRFLMGSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQA  
GASASSSIVVEVLRILVLIGQILFSLAAVFLCLVIKKYLIGPYRKLHMESKGNKEILILGI  
SAFIFLMLTVTEL LDVSMELGCFLAGALVSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHV  
FPTFVAYELTVLVFTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR  
ARRAGVISREVYLLILSVTTLSLLLAPVLWRAAITRCVPRPERRSSL

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,  
576-598, 641-660**N-glycosylation sites.**

amino acids 104-108, 174-178, 206-210, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 55-59, 673-677

**Tyrosine kinase phosphorylation site.**

amino acids 407-414

**N-myristoylation sites.**amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,  
442-448, 525-531, 530-536**Cell attachment sequence.**

amino acids 404-407



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**FIGURE 231**

GAGAAAAACAACAGGAAGCAGCTTACAACTCGGTGAACAACTGAGGGAACCAAACCAGAGAC  
GCGCTGAACAGAGAGAATCAGGCTCAAAGCAAGTGGAAGTGGGCAGAGATTCCACCAGGACTG  
GTGCAAGGCGCAGAGCCAGCCAGATTTGAGAAGAAGGCCAAAAAGATGCTGGGGAGCAGAGCTG  
TAATGCTGCTGTTGCTGCTGCCCTGGACAGCTCAGGGCAGAGCTGTGCCTGGGGGCAGCAGCC  
CTGCCTGGACTCAGTGCCAGCAGCTTTCACAGAAGCTCTGCACACTGGCCTGGAGTGCACATC  
CACTAGTGGGACACATGGATCTAAGAGAAGAGGGAGATGAAGAGACTACAAATGATGTTCCCC  
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGGACAACAGTCAGTTCTGCTTGC  
AAAGGATCCACCAGGGTCTGATTTTTTATGAGAAGCTGCTAGGATCGGATATTTTCACAGGGG  
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTTCATGCCTCCCTACTGGGCCTCAGCC  
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCCAAGCCTCAGTCCCAGCC  
AGCCATGGCAGCGTCTCCTTCTCCGCTTCAAAATCCTTCGCAGCCTCCAGGCCTTTGTGGCTG  
TAGCCGCCCGGGTCTTTGCCCATGGAGCAGCAACCCTGAGTCCCTTAAAGGCAGCAGCTCAAGG  
ATGGCACTCAGATCTCCATGGCCCAGCAAGGCCAAGATAAATCTACCACCCCAGGCACCTGTG  
AGCCAACAGGTTAATTAGTCCATTAATTTTAGTGGGACCTGCATATGTTGAAAATTACCAATA  
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTTATTAGATGGGAAGGGAAATT  
TGGGGATTATTTATCCTCCTGGGGACAGTTTGGGGAGGATTATTTATTGTATTTATATTGAAT  
TATGTACTTTTTTCAATAAAGTCTTATTTTTTGTGGCTAAAAAAAAAAAAA

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**FIGURE 232**

MLGSRAVMLLLLLPWTAAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDEE  
TTNDVPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSSLPDSPVGQLHA  
SLLGLSQLLQPEGHHWETQQIPSLSPSPWPQRLLLRFKILRSLQAFVAVAAARVFAHGAATLSP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Casein kinase II phosphorylation site.**

amino acids 64-67

**N-myristoylation sites.**

amino acids 25-30, 81-86, 122-127

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**FIGURE 233**

CCCACGCGTCCGGCCCTGTAACCAAGATACTGACTGAACATGGCTGGCGGACTCAGGCTGGGGTCTGCAGTGCAG  
CATTAAATGGGCCGCTGACATGAATATGGAGTAGTTTTCTCTAGCAAAGAGTAATGTGGGCCATGGAGTCAGGCCA  
CCTCCTCTGGGCTCTGCTGTTTCATGCAGTCCTTGTGGCCTCAACTGACTGATGGAGCCACTCGAGTCTACTACCT  
GGGCATCCGGGATGTGCAGTGGAACTATGCTCCCAAGGGAAGAAATGTATCAGCAACCAGCCTCTGGACAGTGA  
CATAGTGGCTTCCAGCTTCTTAAAGTCTGACAAGAACCAGATAGGGGGAACCTACAAGAAGACCATCTATAAAGA  
ATACAAGGATGACTCATACACAGATGAAGTGGCCAGCCTGCCTGGTTGGGCTTCCCTGGGGCCAGTGTTCAGGC  
TGAAGTGGGGGATGTCATTCTTATTCACCTGAAGAATTTTGCCACTCGTCCCTATACCATCCACCCTCATGGTGT  
CTTCTACGAGAAGGACTCTGAAGGTTCCCTATACCCAGATGGCTCCTCTGGGCCACTGAAAGCTGATGACTCTGT  
TCCCCCGGGGGGAGCCATATCTACAACCTGGACCATTCCAGAAGGCCATGCACCCACCGATGCTGACCCAGCGTG  
CCTCACCTGGATCTACCATTCTCATGTAGATGCTCCACGAGACATTGCAACTGGCCTAATTGGGCCTCTCATCAC  
CTGTAAAGAGGAGCCCTGGATGGGAACCTCCCTCCTCAACGCCAGGATGTAGACCATGATTTCTTCTCTCTCTT  
CAGTGTGGTAGATGAGAACCTCAGCTGGCATCTCAATGAGAACATTGCCACTTACTGCTCAGATCCCTGCTCAGT  
GGACAAAGAAGATGAGACATTTCCAGGAGAGCAATAGGATGCATGCAATCAATGGCTTTGTTTTGGGAATTTACC  
TGAGCTGAACATGTGTGCACAGAAACGTGTGGCCTGGCACTTGTGGCATGGGCAATGAAATTGATGTCCACAC  
AGCATTTTTCCATGGACAGATGCTGACTACCCGTGGACACCACACTGATGTGGCTAACATCTTCCAGCCACCTT  
TGTGACTGCTGAGATGGTGGCCTGGGAACCTGGTACCTGGTTAATTAGCTGCCAAGTGAACAGTCACTTTCGAGA  
TGGCATGCAGGCACTCTACAAGGTCAAGTCTTGTCCATGGCCCCCTCCTGTGGACCTGCTCACAGGCCAAGTTCG  
ACAGTACTTCAATTGAGGCCCATGAGATTCAATGGGACTATGGCCCCGATGGGGCATGATGGGAGTACTGGGAAGAA  
TTTGAGAGAGCCAGGCAGTATCTCAGATAAGTTTTTCCAGAAGAGCTCCAGCCGAATTGGGGGCACTTACTGGAA  
AGTGGCATATGAAGCCTTTCAAGATGAGACATTCCAAGAGAAGATGCATTTGGAGGAAGATAGGCATCTTGAAT  
CCTGGGGCCAGTGATCCGGGCTGAGGTGGGTGACACCATTAGGTGGTCTTCTACAACCGTGCCTCCAGCCATT  
CAGCATGCAGCCCATGGGGTCTTTTATGAGAAAGACTATGAAGGCACTGTGTACAATGATGGCTCATCTTACCC  
TGGCTTGGTTGCCAAGCCCTTTGAGAAAGTAACATACCGCTGGACAGTCCCCCTCATGCCGTCCTCATGCTCA  
GGATCTGCTTGTCTCACTTGGATGTACTTCTGTCTGCAGATCCCATAGAGACACAAATTCTGGCCTGGTGGG  
CCCGCTGCTGGTGTGCAGGGCTGGTGCCTTGGGTGCAGATGGCAAGCAGAAAGGGGTGGATAAAGAATTTCTTCT  
TCTCTTCACTGTGTGGATGAGAACAAGAGCTGGTACAGCAATGCCAATCAAGCAGCTGCTATGTTGGATTTCCG  
ACTGCTTTTCAGAGGATATTGAGGGCTTCCAAGACTCCAATCGGATGCATGCCATTAATGGGTTTCTGTTCTCTAA  
CCTGCCCAGGCTGGACATGTGCAAGGGTGACACAGTGGCCTGGCACCTGCTCGGCCTGGGCACAGAGACTGATGT  
GCATGGAGTCATGTTCCAGGGCAACACTGTGCAGCTTCAGGCGATGAGGAAGGGTGCAGCTATGCTCTTTCCCTCA  
TACCTTTGTCTATGGCCATCATGCAGCCTGACAACCTTGGGACATTTGAGATTTATTGCCAGGCAGGCAGCCATCG  
AGAAGCAGGGATGAGGGCAATCTATAATGTCTCCAGTGTCTGGCCACCAAGCCACCCCTCGCCAACGCTACCA  
AGCTGCAAGAATCTACTATATCATGGCAGAAGAAGTAGAGTGGGACTATTGCCCTGACCGGAGCTGGGAACGGGA  
ATGGCACAACCAGTCTGAGAAGGACAGTTATGGTTACATTTTCTGAGCAACAAGGATGGGCTCCTGGGTCCAG  
ATACAAGAAAGCTGTATTACAGGAATACACTGATGGTACATTAGGATCCCTCGGCCAAGGATGGACCAGAAGA  
ACACTTGGGAATCTTGGGTCCACTTATCAAAGGTGAAGTGGTAGATATCCTGACTGTGGTATTCAAGAATTAATGC  
CAGCCGCCCTTACTCTGTGCATGCTCATGGAGTGTAGAATCTACTACTGTCTGGCCACTGGCTGCTGAGCCTGG  
TGAGGTGGTCACTTATCAGTGGAAACATCCAGAGAGGTCTGGCCCTGGGCCAATGACTCTGCTTGTGTTTCTCTG  
GATCTATTATTCTGCAGTGGATCCCATCAAGGACATGTATAGTGGCCTGGTGGGGCCCTTGGCTATCTGCCAAA  
GGGCATCCTGGAGCCCATGGAGGACGGAGTGACATGGATCGGGAATTTGCATTGTTGTTCTTGATTTTTGATGA  
AAATAAGTCTTGGTATTTGGAGGAAAATGTGGCAACCCATGGGTCCAGGATCCAGGCAGTATTAACTTACAGGA  
TGAACTTTCTTGGAGAGCAATAAAATGCATGCAATCAATGGGAACTCTATGCCAACCTTAGGGTCTTACCAT  
GTACCAAGGAGAACGAGTGGCCTGGTACATGCTGGCCATGGGCCAAGATGTGGATCTACACACCATCCACTTTCA  
TGCAGAGAGCTTCTCTATCGGAATGGCGAGAACTACCGGGCAGATGTGGTGGATCTGTTCCAGGGACTTTTGA  
GGTTGTGGAGATGGTGGCCAGCAACCCTGGGACATGGCTGATGCACTGCCATGTGACTGACCATGTCCATGCTGG  
CATGGAGACCCTCTCACTGTTTTTTCTCGAACAGAACTTAAGCCCTCTCACCCTCATACCAAAGAGACTGA  
AAAAGTGGCCCCCAGAGACATTGAAGAAGGCAATGTGAAGATGCTGGGCATGCAGATCCCCATAAAGAATGTTGA  
GATGCTGGCCTCTGTTTGGTTGCCATTAGTGTCAACCTTCTGCTCGTTGTTCTGGCTCTTGGTGGAGTGGTTG  
GTACCAACATCGACAGAGAAAGCTACGACGCAATAGGAGGTCCATCCTGGATGACAGCTTCAAGCTTCTGTCTTT  
CAAACAGTAACATCTGGAGCCTGGAGATATCCTCAGGAAGCACATCTGTAGTGCATCCAGCAGGCCATGGACT  
AGTCACTAACCCCACTCAAAGGGGCATGGGTGGTGGAGAAGCAGAAGGAGCAATCAAGCTTATCTGGATATT  
CTTTCTTTATTTATTTTACATGGAAATAATATGATTTCACTTTTTCTTTAGTTTCTTTGCTCTACGTGGGCACCT  
GGCACTAAGGGAGTACCTTATTATCCTACATCGCAAATTTCAACAGCTACATTATATTTCTTCTGACACTTGA  
AGGTATTGAAATTTCTAGAAATGTATCCTTCTCAAAAGTAGAGACCAAGAGAAAACTCATTGATTGGGTTTCT  
ACTTCTTTCAAGGACTCAGGAAATTTCACTTTGAGTGGGCCAAGTGAGCTGTTAAGATAACCCACACTTAAAC  
TAAAGGCTAAGAATATAGGCTTGTGGGAAATGAAGGTAGGCTGAGTATTGGGAATCCAAATTGAATTTTGATT  
CTCCTTGGCAGTGAACCTTTTGAAGAAGTGGTCAATGGGTTGTTGCTGCCATGAGCATGTACAACCTCTGGAGC  
TAGAAGCTCCTCAGGAAAGCCAGTTCTCAAGTTCTTAACCTGTGGCACTGAAAGGAATGTTGAGTTACCTCTTC  
ATGTTTTAGACAGCAACCCATATCCATTAAAGTACTTGTAGACCAAAAAAAAAAAAA

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**FIGURE 234**

MWAMESGHELLWALLFMQSLWPQLTDGATRVYYLGIIRDVQWNYAPKGRNVITNQPLDSDIVASS  
 FLKSDKNRIGGTYYKTIYKEYKDDSYTDEVAQPAWLGFLGPVLQAEVGDVILHLKNFATRPY  
 TIHPHGVFYEKDSEGLYPDGSSGPLKADDSVPPGGSHIYNWTIPEGHAPTADAPACLTWIIYH  
 SHVDAPRDIATGLIGPLITCKRGALDGNSPQQRQDVDHDFLLFSVVDENLSWHLNENIATYC  
 SDPASVDKEDETFOESNRMHAINGFVFGNLPENMCAQKRVAWHLFGMGNEIDVHTAFFHGQM  
 LTTRGHHTDVANIFPATFVTAEMVPWEPGTWLISCQVNSHFRDGMQALYKVKSCSMAPPVDLL  
 TGKVRQYFIEAHEIQWDYGPMGHDGSTGKNLREPGSISDKFFQKSSSRIGGTYYWKVRYEAFQD  
 ETFQEKMHLEEDRHLGILGPVIRAEVGDTIQVVFYNRASQPFSMQPHGVFYEKDYEGTVYNDG  
 SSYPGLVAKPFKVTYRWTVPPHAGPTAQDPACLTWMYFSAADPIRDTNSGLVGPLLVCRAGA  
 LGADGKQKGVDEKFFLLFTVLDENKSWYNSANQAAAMLDFRLLSEIEGFQDSNRMHAINGFL  
 FSNLPRLDCKGDTVAWHLLGLGTETDVHGVFMFGNTVQLQGMKGAAMLFPHTFVMAIMQPD  
 NLGTFEIYCQAGSHREAGMRAIYNVSQCPGHQATPRQRYQAARIYYIMAEVEWDYCPDRSWE  
 REWHNQSEKDSYGYIFLSNKDGLLSRYKKAVFREYTDGTFRI PRPRTGPEEHLGILGPLIKG  
 EVGDILTUVFKNNASRPYSVHAHGVLESTTVWPLAAEPGEVVTYQWNI PERSGPGPNDACS  
 WIYYSAVDPIKDMYSGLVGPLAICQKGILEPHGGRSDMDREFALLFLIFDENKSWYLEENVAT  
 HGSQDPGSINLQDETFLSNKMHAINGKLYANLRGLTMYQGERVAWYMLAMQDQVDLHTIHFH  
 AESFLYRNGENYRADVDLFPGTFEVEMVASNPGTWLMHCHVTDHVVHAGMETLFTVFSRTEH  
 LSPLTVITKETEKVPPRDIEEGNVKMLGMQIPIKNVEMLASVLVAISVTLLLVVLALGGVVWY  
 QHRQRKLRRNRRSILDDSFKLLSFKQ

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 1109-1130

**N-glycosylation sites.**

amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,  
876-880, 934-938

**Glycosaminoglycan attachment site.**

amino acids 871-875

**Tyrosine kinase phosphorylation sites.**

amino acids 82-90, 137-145, 494-502, 513-521

**N-myristoylation sites.**

amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,  
843-849

**Multicopper oxidases signature 1.**

amino acids 344-365, 696-717, 1043-1064

**Multicopper oxidases signature 2.**

amino acids 1048-1060

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**FIGURE 235**

GGAAAGAGTGCTGGTACTACAACCAGGAAGTGACAGATAATGTGCTTTAACTACATTAGAAAAGCTTCTCATAG  
CAAACTGAGAGATTGAAGCAGTGATTATTTTTACATAGTTGTCTTAAATATTTGGAGCTCTGCTGTGCATAGA  
GATGGCAACATACTTAGAATACACAGCTTTCTGGGCCAGAAATTGATCTTCTGACTTTTGAGCCTTATCTGATTA  
CTGCTTGGTTTCATCTTTATTTTGTAACTACTCTGTAGGCTGAAAGGGAGAGACTCTCCTTGGTTTGCAGAGCC  
TGACTAGACAGGAATTCGGCAACTGCTCCAGCAGAACTATGGCACTGAGCTAGGTTTAAATGCTGAGGAGATGG  
AAAACTTGTCACTGTCGATTGAGGATGTGCAGCCAAGAAGTCCAGGAAGAAGCAGCTTGGATGACTCTGGGGAGA  
GAGATGAAAAATTATCCAAGTCAATCAGTTTTTACCAGTGAATCAATTAGTCGGGTTTTCAGAAACAGAGTCATTCTG  
ATGGAAATTCATCAAAAGGAGGATTAGGCAAGAGGAGTCCCAAAATGAGAAACAGACCAAAAAGAGTCTCTTAC  
CAACTTTGGAAAAGAAGTTAACTAGAGTGCCATCAAGTCACTGGACTTGAATAAAAATGAATATCTTTCTCTGG  
ACAAAAGCAGCATTTCAGATTCTGTTGATGAAGAAAATGTTTCTGAGAAAGATCTTCATGGAAGACTTTTTATCA  
ACCGTATTTTTCATATCAGTGCTGACAGAATGTTGAATTGCTCTTTACCAGTTCACGCTTTATGCAGAAATTTG  
CCAGTTCTAGAAATATAATAGATGTAGTATCTACCCCTTGGACTGCAGAACTTGGAGGTGATCAGCTGAGAACGA  
TGACCTACACTATAGTCCCTTAATAGTCCACTTACTGGAAAATGCACTGCTGCCACTGAAAAGCAGACACTGTATA  
AAGAAAGTCGGGAAGCAGGATTTTATTTGGTAGATTCAGAAGTACTGACACATGATGTCCCCTACCATGATTACT  
TCTATACCGTGAACAGATACTGTATCATCCGATCTTCAAAACAGAAATGCAGGCTAAGAGTTTCCACAGATTTGA  
AATACAGAAAACAGCCATGGGGCCTTGTCAAATCTTAAATTGAAAAGAATTCTTGGAGTTCTTTGGAGGACTATT  
TCAAAACAGCTTGAATCAGATTGTGAATTGAAGAATCTGTATTAAATCAGGCCATTGAAGACCCTGGAAAACCTTA  
CTGGCCTACGAAGGAGAAGGCGAACCTTCAACCGAACAGCAGAAACAGTTCCCTAACTTTCCTCTCAGCATTCCT  
CTGGAGATGTGGGCTTAGGTGCCAAAGGGGATATTACAGGAAAGAAAAGGAAATGGAAAACATAACGTCACCTC  
TTATTGTGGAATGAGTATTTTTGTGTTGTTATTAGTTTTGTTGAATGTGACACTGTTTCTGAAGCTGTCAAAGA  
TAGAACATGCTGCTCAGTCCTTTTACCGTCTCCGCCTCCAAGAAGAGAAATCTTTAAATTTAGCCTCTGATATGG  
TGTCAGAGCAGAACTATTCAGAAGAATAAAGATCAGGCCATCGTTTAAAGGGAGTGCTCCGAGACTCCATAG  
TGATGCTTGAACAGCTGAAGAGCTCACTCATTATGCTTCAGAAAACGTTTGATCTACTAAATAAGAATAAGACTG  
GCATGGCTGTTGAAAGCTAGTGATCTGAAGGACTAAAACCGCAGAGATACTTGGAACTTAAAGAAAATACCTGGA  
AGAAAACAGACGAATGAAGGATTTTGGCATAGAACATTTCTATGTTTTTTCATTATTGAGATTTCTAATATGAA  
CATTTCTTTCAGTAACATTTATTTGATAATTAGTTTCTGCTGGCCTTAATAATCCATCCTTTCACCTCTTATAGA  
TATTTTTAAGCTGTGAATTTCTTCAGTGAACCATGAAATATATTATAGAAGTGAATTTCTCTGATACAAAAGAA  
AATGACACACCCTGAATTGAGTGGTATGGTCTCATTCTACAGTGAAGTCTGATGCTTTGTTAGCACAGAATCCG  
TACATGTCCAATAGGTCGCTTTTGTAACTGAGATAAGACCAAGAGGATAAACAGGACAATATAAGAAGAAACCTC  
TATGTCATTACTGATTTTTAAAGGTTCTGTTTTCAGGCATATAACATTTCCAGGTTTGTGTACTGTAAAGATTATA  
ATGTCTTCATTTATTTTAGCATGCAAATTTAATAGTCAAACCTTTTTGAATCTGCATGTTGATGATGATTATCAGAA  
AGGGTCTTCTGCCATGCTGTATCTTTATGAAAGAAATAGTTGTTTTTCTTAAGGTAACATCAGAGGTGGGATT  
ATCTTGCCCTCCTCACTTAGAATACCAACAGTCAAAGGAAGAACCATCCTCTGAGTTTTAAAAACAGAAAGGTTA  
TGTTAAATCTGGGCATTTAGTGACAGATCAAATGCATACTTGAACCTAAGATTGGCTTCAGCTTAGCAGTCTTTC  
ATGGTGGAAGTGACACATCTGGTTGAAAATAATTTGTGATTTTTCAGTAACCATGTATGGCTTCCTTCTTTATGT  
ATGTGTGTGACTTGTTTTAATTGGTAAGTTATAAGCCAGACATAGATTTTAGCTCTTAAATAAAAACTTCAGGGG  
CACGTATGTCCAGTACAAGTGTACTGACTATCAAGTTTTAACTCAGATGCAAGCTTTGGCTCTTTCATAAAAAG  
TTTTTATGCATATGTGTCTCCATACAAGTGGCTCATTTAAATAAGAAGCTTTGTAACTGACTTAAATCAGATAT  
TTTTTCAAGAGTTAGGGAAAGTTGAAGTGTCTTACTGTTTTGTCTCTTGAGCCCTTTCTCTGGGGAAAAAATACA  
TATCCATCTATCTATCTATATATAAACTGTGTATACATTCTTACTGTTTGAACAACTATTGCCTTTAATTAAATG  
TTTCATTTTTCTCCAGAGTCCCCAAAGCCACATGGCATTTATATAGTCATTTTTGAGATGCCTGTAGAGAATGAA  
AGTATTGACTCCGTTAGAGGGAAAATGGGTTTCTCTGGGTGAATTTCCAACGAAGCATACCTAGGGGTAAACAGTGA  
ACCTACCTGGGTTTGTGTTTTGTTTGGTAAGGATTTATGTAGTGTCTGGCTGTAAGCAAGAATGAGTGGATTATAA  
ACTTGAAGATTTCTCTGTTAAAGTCACAAAATGATCGACAAACAATATTTTTGTGATGTTTATTTAAACGTTGT  
ATTTTATAACATACTTCAAGGAAGAGTATCGAAGTAAGTTGCTTTATAAATTAAGACTAAATTCGTATGGATGCA  
GAATTCATTAATAAAATTTGAGCCTGTTACGTAAATGAATATTAATAAAATTTGAAAATTTCAAAA

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**FIGURE 236**

MENLSLSIEDVQPRSPGRSSLDDSGERDEKLSKISFTSEISRVSETESFDGNSSKGGLGKE  
ESQNEKQTKKSLPTLEKKLTRVPSKSLDLNKNEYLSDKSSTSDSVDEENVPEKDLHGRLFI  
NRIFHISADRMFELLFTSSRFMQKFASSRNIIDVVSTPWTAEELGGDQLRTMTYTIVLNSPLTG  
KCTAATEKQTLTKESREARFYLVDSVLTHDVPYHDYFYTVNRYCIIRSSKQKCRRLRVSTDLK  
YRKQPWGLVKSLIEKNSWSSLEDYFKQLESLLIEESVLNQAIEDPGKLTGLRRRRRTFNRTA  
ETVPKLSSQHSSGDVGLGAKGDITGKKKEMENYNVTILIVVMSIFVLLLVLNVTFLKLSKIE  
HAAQSFYRLRLQEEKSLNLASDMVSRAETIQKNKDQAHRLKGVLRLDSIVMLEQLKSSLIMLQK  
TFDLLNKNKTGMARES

**Transmembrane domain:**

amino acids 352-371

**N-glycosylation sites.**

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 81-85, 307-311

**Tyrosine kinase phosphorylation sites.**

amino acids 202-211, 246-254, 341-349

**N-myristoylation site.**

amino acids 259-265

**Amidation site.**

amino acids 339-343

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**FIGURE 237**

CAGGGGCTGGAGGGCAGGGGAGGGGGATGATGTCATTCCTGCTCGGCGCAATCCTGACCCTGCT  
CTGGGCGCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTTCAATGCTGAAAAGTTCTC  
AGGCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGTCTTCCTGGGCAAGAAGGACCA  
CCTGTCCATGTCCACCAGGGCCATCAGGCCCCACAGAGGAGGGCGGCCTCCACGTCCACATGGA  
GTTCCCGGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGGCTCCGAGGG  
ACACTTCAGAGTCCCGGCCTTGGGCTACCTGGACGTGCGCATCGTGGACACAGACTACAGCTC  
CTTCGCCGTCCTTTACATCTACAAGGAGCTGGAGGGGGCCCTCAGCACCATGGTGCAGCTCTA  
CAGCCGGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTTCCAGGACTTCTACCCGACCCT  
GGGGCTCCCCAAGGACATGATGGTCATGCTGCCCCAGTCAGATGCATGCAACCCTGAGAGCAA  
GGAGGCGCCCTGACACCTCCGGAGCCCCACCCCCGCCCTTCCCAGGTGGAGCCAAAGCAGCAG  
GCGCCTTTGCCCTGGAGTCAAGACCCACAGCCCTCGGGGACCACCTGGAGTCTCTCCATCCT  
CCACCCCCCGCCTGTGGGATGCCTTGTGGGACGTCTCTTTCTATTCAATAAACAGATGCTGCA  
GCCTCA

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## **FIGURE 238**

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMASDCRVFLGKKDHLMSSTRAI  
RPTEEGGLHVHMEFPGADGCNQVDAEYLKVGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK  
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

**Signal peptide:**

amino acids 1-20

**Tyrosine kinase phosphorylation site.**

amino acids 110-117

**N-myristoylation sites.**

amino acids 7-13, 79-85, 130-136

**Amidation site.**

amino acids 50-54



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**FIGURE 239**

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCCGAGGCGGTTCA  
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGGCGTGGATATGGAGCTGGCTGCT  
GCCAAGTCCGGGGCCCCGCGCCGCTGCCTAGCGCGTCTGGGGACTCTGTGGGGACGCGCCCCG  
CGCCGCGGCTCGGGGACCCGTAGAGCCCGGCGCTGCGCGCATGGCCCTGCTCTCGCGCCCCG  
GCTCACCTCCTGCTCCTCCTCATGGCCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACCAC  
CGACTGGAGAGCCACCCTGAAGACCATCCGGAACGGCGTTCATAAGATAGACACGTACCTGAA  
CGCCGCCTTGACCTCCTGGGAGGCGAGGACGGTCTCTGCCAGTATAAATGCAGTGACGGATC  
TAAGCCTTTCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT  
TGGTGTTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTTGCAACCAACACGACAGGTG  
CTATGAGACCTGTGGCAAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCCAA  
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTCAAGCATGTGAAACAAC  
AGTGGAGCTCTTGTTTGACAGTGTTATACATTTAGGTTGTAAACCATATCTGGACAGCCAACG  
AGCCGCATGCAGGTGTCATTATGAAGAAAAAACTGATCTTTAAAGGAGATGCCGACAGCTAGT  
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAACT  
GTCTTATTTTTGTGAAAGGATTATTTTGAGACCTTAAATAATTTATATCTTGATGTTAAAC  
CTCAAAGCAAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCAGCTTGTCTTCTCAGGTATCTT  
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAACAAGTGCTT  
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAAA  
AAAAGAGATCAAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGGAAAATGG  
GGAAATTATCACTTACAAGTATTTGTTTACTATGAAATTTTAAATACACATTTATGCCTAGAA  
GGAACGGACTTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAAGTACAACATAATAT  
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA  
GGACAAGGTTTCCATTTTCCAGTTGTAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG  
CAACCCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTTCAGAA  
GCATAGCCACTCCCATTTTATGAGCTACTCACATGACAAATGTCATCTTTTGCTATAACCTTT  
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

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## **FIGURE 240**

MALLSRPALTLLLLLLMAAVVRCQEQAQTTDWRATLKTIRNGVHKIDTYLNAALDLLGGEDGLC  
QYKCS DGSKPFPRYGYKPSPPNGCGSPLFGVHLNIGIPSLTKCCNQHDRCYETCGKSKNDCDE  
EFQYCLSKICRDVQKTLGLTQHVQACETTVELLFDSVIHLGCKPYLDSQRAACRCHYEKTDL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites:**

amino acids 57-63, 93-99

**Phospholipase A2 histidine active site:**

amino acids 106-114

**Neuraxin and MAP1B proteins repeat proteins Block:**

amino acids 109-137

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**FIGURE 241**

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCCGGCCGTT  
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC  
GTCTGCCGCTATCTCCGCCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG  
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCACGGACGGGGCGCCGCGCAGCTGCCTC  
TCGTGCTCACC GCGCTGTGGGCCGCGGCCGTGGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG  
GTCCCGGGCCGCGCCGCTGGGACCCCTGGCCCGGGCCTTGCAGCTGGCGCTGGCCGCCTTCC  
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCCTGCGCTCGGATCCCAGCATCCGTGGCG  
TGATGCTGGCCGGCCGCGGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG  
TGCCGCCACGCAGCGGACACTGCTCTGCCTGCCGCGTCTGCATCCTGCGTCGGGACCACCACT  
GCCGCCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCCTGTGCCTGCTGCTTC  
ATGCCGCCGGCGTCCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCACTGTCGGCCCTGCTGC  
GAGCCCACAGCCCCCTCCACATGGCTGCCCTCCTCCTGCTTCCCTGGCTCATGTTGCTCACAG  
GCAGAGTGTCTCTGGCACAGTTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC  
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG  
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG  
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCCTGGCCTCCCCATTGCCTGGGGATGGGA  
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTGACTCCAGGAAGAGCCAGAGC  
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT  
GGACCTTAACATCTGCATTGGACAACCTCCACCCCTTCCTTGGCCTTGCCCCTGCCCGCCTACA  
CTCCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG  
GGGCTGCTCAGGCCGCCTAGCTGCCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA

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**FIGURE 242**

MGQPWAAGSTDGAPAQPLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL  
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCR  
LGRCVGFGNYRPFCLLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLLPWLMLLTGRV  
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSYDLGPCHNLQAALGPR  
WALVWLWPF LASPLPGDGITFQTTADVGH TAS

**Important features:****Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 51-66,143-160,174-191,198-214

**N-myristoylation sites:**

amino acids 2-8,8-14,30-36,81-87,88-94,90-96,206-212

**Leucine zipper pattern:**

amino acids 143-165,150-172,157-179,164-186

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**FIGURE 243**

CTTGTCTTTGTGTCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTTCTCTCGGACGCTCTC  
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCCCTTCCCGGCTTCC  
TTCGCTACCGGGGACGCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTCAT  
CTTCTCAAGAGTTCGCCCCCTCTGGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT  
CTGTGAACTCCGTCTCACACCATCCCGCCATCTTCTCTGCCTTGGCCCCCTTTTCTCTGTACAG  
CCAGCTCTGTGTCCTTTTTCTTCTCCCCCTCTAAAATCGACTCCTCTTCTCCCTGAGAGCCCCA  
CCTTTGTGCCCCACTCCTCATTTTCCTACGCCTCCCTCTCTCTGCTGGTCCCTCTCTCTCCCTG  
CAAGGTTCCATTCCATCAATTTGTTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT  
CCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTTGAGGATTTCACTTCAATCTTTTCTGGT  
TGCCTCTCCACTTGTACTCAGCTTGTTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC  
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCCGTGAGATCTGTTGTCAGCCTTC  
GTTTCTCTTTCCTGTGTCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTT  
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGGTGGCCGACGTGACCTCT  
AGCTGGACTGCTGGGCAGGGGAGCTGTCCTAGATAAAATTGGAAGAAACAGTGACCCAGAGA  
CAGGTGGACAAAGAATTGCGGGACTGATGGGAAGTGAAGTGGGATCCAGACTGAAACTGATT  
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGCCATGGGACCCAGCATTTGAGACT  
TGTGCAGCTGTTCTGCCTTCTAGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG  
CTATGAAGCAACAGCCTCAAGATTCAAGAGCTGTTGCTTTCCATAACTGGAAGTGGCTTCTGAT  
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTCAATTGAGACAGG  
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTCGTCTTACCCTGCGCAAAAT  
CTCCTACCTTGTTTCCCCACCCGGAGTGTCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA  
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC  
TATCACATCTGCGTCCCTGTAGCTGCCCCGACCTGTGTGGGCGAGCACATGAAGGATTGCCTCCC  
AAATTTTGTCAACCACTAATTCTTGCCCCTTGGCTGCTTCTACGTGTTACAGTTCCACCTTAAA  
ATTTCAAGCAGGGTTTCTCAATACCACCTTCCTCCTCATGGGGTGTGCTCGTGAACATAACCA  
GCTTTTAGCAGATTTTCATCATATTGGGAGCATCAAAGTGACTGAGGTCCTCAACATCTTAGA  
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTTGGGGTGTGCTCTTAGG  
CCTCCTGTTTGCCTTCAGGGACTTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTTCA  
CATAACAAATAAAATAGCAGAGTTCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

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**FIGURE 244**

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE  
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK  
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSSTLKFAQAGFLNTTFLLM  
GCAREHNQLLADFHHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation sites:**

amino acids 117-121, 183-187

**N-myristoylation sites:**amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,  
235-241, 239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

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**FIGURE 245**

GTGGAGTTGGGTGGTGTCTGGGAGCCTCTCCCTGAGGGGCACCGCGTCTTCAGGAGCTGGGCCTCCAGTGC GGCGC  
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGGCCGTGGCGCTGGGCGGCTGCGGGGCCTGACCGG  
TCCGCTCATGGTGCCGCCACGACGCCATCGCGGGGCAGGAAGGCCAGGGGTGCTGAGTTCCTCACCTCCTTTTAG  
ACTGAGATCTGCCAAGTTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAAATGGT  
GTGTGTATTTGTCATGAACCGAATGAATTC CAGAACAGTGGTTTCACTCAGCGCAGGCGAATGGCTCTTGGGAT  
TGTTATTCTTCTGCTTGTTGATGTGATATGGGTTGCTTCCTCTGAACCTACTTCGTATGTTTTTACCCAGTACAA  
CAAACATTCTTCAGCACCTTTGCAAAAACATCTATGTTTGT TTTGTACCTTTTGGGCTTTATTATTTGGAAGCC  
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTTGCAGATGCTGAAGGTTACTTTGC  
TGCTTGCAACAGATACAACATGAATAGTTCTTTGAGTGAACCTCTGTATGTGCCTGTGAAATTCATGATCT  
TCCAAGTAAAAACCTGAGAGCACAAACATTGATACTGAAAAAACCCCAAAAAGTCTCGTGTGAGGTT CAGTAA  
TATCATGGAGATTCGACAGCTTCCGTCAAGTCATGCATTGGAAGCAAAGTTGTCTCGCATGT CATATCCTGTGAA  
AGAACAAGAATCCATACTGAAAACTGTGGGAAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTTTTTG  
CTTTGTGTGGTTTTTTGGCAAATTTGTCATATCAAGAAGCACTTTCAGACACACAAGTTGCTATAGTTAATATTTT  
ATCTTCAACTTCCGGACTTTTTACCTTAATCCTTGCTGCAGTATTTCCAAGTAACAGTGGAGATAGATTTACCTT  
TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGTACTGGTAAACCTGGCAGGGTCTGAAAAACCTGC  
TGGAAGAGACACAGTAGGTTCCATTTGGTCTCTTGCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA  
GAGAAAAGTAGATAGAGAAGACAAGTTGGATATTCCAATGTTCTTTGGTTTTGTAGGTTTGT TTAATCTGCTGCT  
CTTATGGCCAGGTTTTCTTTTACTTCATTATACTGGATTTGAGGACTTCGAGTTTCCCAATAAAGTAGTATTAAT  
GTGCATTATCATTAATGGCCTTATTGGAACAGTACTCTCAGAGTTCCTGTGGTTGTGGGGCTGCTTTCTTACCTC  
ATCATTGATAGGCACACTTGCACTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAAGGT  
GCAGTTTTCTTGTTATTTTTTG CAGGAGCTATCCCTGTATTTTTTTTCA TTTTTTTATTGTAACTCTCCTATGCCA  
TTATAATAATTGGGATCCTGTGATGGTGGGAATCAGAAGAATATTTGCTTTTATATGCAGAAAACATCGAATTC A  
GAGAGTTCAGAAGACAGCGAACAGTGTGAGAGTCTCATTTCTATGCACAGTGT TTTCTCAGGAGGATGGAGCTAG  
TTAGCTGTCTGTTGTCTGTAGCCAGCTTGATAATGGAAC TATACAGCGAAGAGACAATCTCTGGCAAGTTTTTG  
TAGAAAAATGTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTTCTTTGAAACTCTAAAATATATTTTTTCTC  
ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG  
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTTGA  
ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTTACATGT TAAATGCTGGAATATATTATGAAAAAT  
GTTTTCAAGAAATCACTTAAGTGTT CATAGACCAGTATTTCTGACAGGTAAAATGCTAAAATAAGCTACCTGTAA  
TAAGTGTGGATTATATTTTTGGGTTTTGTAGAATATTGCAAATTAACCACACAAAAAATGTTTAATTTATGCAAC  
AAGCATGTTTGTGCAAAATTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAAATATCTGGTTCACTTACACTA  
CATTTACTGTATTATCTTTTATAGCATTAGTGCCTTG TATTTTAAATCTGTGACAAACCATGGCAAATTTTTTA  
AAGGGGAAGTATTATTATAAAATGAAGAAATATG TATTTCTAAAGGCTATATTGCTGTAAACTTAATTGATAAAG  
CTCTGTTTAATTTAGAGTTTTGAAGAAATAGTCTCCCTTCAATTAAGAAATTTTCATAATGGAATGATTTAAAT  
GAAGTGACAAAGAGTATTATTAAAAATACAATGTTTATAAAAAA

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**FIGURE 246**

MVPPRRHRGAGRPGVLSSSPFRLRS AKFSGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF  
TQRRRMALGIVILLLLVDVIWVASSELTSYVFTQYNKPPFFSTFAKTSMEVLYLLGFIIWKPWQR  
QCTRGLRGKHAAFFADAEGYFAACTTDTMNSSLSEPLYVPVKFHDLPSEKPESTNIDTEKTP  
KKSRVRFSNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF  
LANLSYQEALSDTQVAIVNILSSTSGLFTLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN  
LAGSEKPAGRDTVGSIWLAGAMLYAVYIVMIKRKVDREDKLDIPMFFGFVGLFNLLLLWPGE  
FLLHYTGFEDEFEPNKVVLMCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALSLTIPLSIIA  
DMCMQKVQFSWLF FAGAIPVFFSFFIVTLLCHYNNWDPVMVGIRRIFAFICRKHRIQRPEDS  
EQCESLISMHSVSQEDGAS

**Important features:****Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,  
364-379, 399-419, 453-472

**N-glycosylation sites:**

amino acids 157-161, 255-259

**N-myristoylation sites:**

amino acids 14-20, 329-335, 404-410, 407-413, 418-424



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**FIGURE 247**

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCCTGAAGACAGAGGG  
CAGAACTCTGAGTTCCAGAACCATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT  
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTTCTAAAACTGAA  
TCCTGCTACTAAAATAATTCAGATGATATATTTTTCCAATTCTACAATCTTGCTTTGTTTTAT  
TTAGTTGTTTTCTCTCTCTCTTCCCAGTTTTCCAGAGACTGGAGCTAAACTGGGCTTTCAACA  
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTTGAATCTGACTGTTGCTTTGGCCTTTAATC  
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT  
GCGCTGGAGTCCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAAGC  
TTCGGGTGATATTGGGGGTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG  
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACTTCTATTGATCATGACATCATGC  
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC  
AACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT  
ACAAAGAGCCCGATTCACTGCAAACTGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTGCGG  
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGTGGGCATTGTGCCAGGAAGGA  
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC  
TGTCTTTTGCGGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT  
ATATACCCTGGATTGAAAATGTAATCCAAAATAACTGAGCTGTGGCAGTTGTGGACCATATGA  
CACAGCTTGCCCCATCGTTCACCTTTAGAATTAAATATAAATTAACCTCCTC

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**FIGURE 248**

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYLKSDYLPAGVLIHPLWVITAAHCNLPKLR  
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKLKTEAELNDYVKLANLPYQT  
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ  
PCKEVSAAAPAICNGMLQGILSFADGCVLRADVGIYAKIFYIIPWIENVIQNN

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites:**

amino acids 11-15,156-160,173-177

**Tyrosine kinase phosphorylation site:**

amino acids 108-117

**N-myristoylation sites:**

amino acids 182-188,203-209

**Amidation site:**

amino acids 185-189

**Serine proteases, trypsin family, histidine active site:**

amino acids 52-58

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**FIGURE 249**

GCGAGGCGGCCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC  
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC  
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT  
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG  
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA  
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG  
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG  
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCA  
ATAAATGTCTCCATACCATCAA

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**FIGURE 250**

MWWLSIGALIGLSVAAVVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV  
NTGMAAEVPKVSPLQQSYSCLNPNQLESNEGQAVNSKRLLLHCFMATVTTSDIPGSPEEASVPN  
PDLGCPVP

**Important features:**

**Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 7-13, 11-17, 62-68, 93-99

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**FIGURE 251**

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG  
GCAGAGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACCATGCGAG  
GCCAGCGGAGCCTGCTGCTGGGCCCCGGCCCGCCTCTGCCTCCGCCTCCTTCTGCTGCTGGGTT  
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT  
GCCTGCGCTCCCTGCTCTACAACTCCTTTGGGGGCAGTGACACCGCTGTTGATGCTGCCTTTG  
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTCGTGGTCCTGG  
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGTCTGCCTCTCATCCTCC  
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA  
TTGTCTTCCACTACTACCAGGCCATCACCCTCCGCCTGGGTACCCACCCCAGGGCAGGAATG  
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCCGAACACACCACT  
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCCTGGCTAAACAATTGTG  
TGGGCCACTATAACCATCGGTACTTCTTCTCTTTCTGCTTTTTTCATGACTCTGGGCTGTGTCT  
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC  
AGACCCCAACACCCACCTTCTCCTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT  
GGTTCCTGTGCAGTTCTGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA  
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTCCGGCTACAGG  
CCAAGGGCAGAGTATTTAGGAATCCTTACAACTACGGCTGCTTGGACAACCTGGAAGGTATTCC  
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACTTGCCCC  
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG  
CAGTGTGAGCTGGACTGTGTGAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTCA  
AGGGCCTCCAAGGGCAGCTTTTCTCAGAATCCTTGATCAAAAAGAGCCAGTGGGCCTGCCTTA  
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTTTACCCTGCAGAAGAAAGACACAATGT  
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAAAACAGAAGTTCCAACCCCAGACTAGG  
GGTCAGGCAGCTAGCTACCTACCTTGCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC  
TGAGATTGGCCACCACCTCTTCTACTTGCTGTCTGAAAAACACCTGACTAGTACAGCTGAGA  
TCTTGGCTTCTCAACAGGGCAAAGATACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA  
TGCTGCTTAAGGGAGCACAAATAAAGGTATTCGATTTTTTAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 252**

MRGQRSLLLGPRLCLRLLLLLGYRRRCPLLRLGLVQRWRYGKVCLRSLLYNSFGGSDTAVDA  
AFEPVYWLVDNVIRWFGVVFVVLVIVLTGSIVAIAYLCVLPLILRTYSVPRLCWHFFYSHWNL  
ILIVFHYYQAITTPPGYPPQGRNDIATVSICKKCIYKPARTHHCSICNRCVLKMDHHC PWLN  
NCVGHYNHRYFFSFCFFMTLGCVCYCSYGSWDLFREAYAAIETYHQTPPPTFSFRERMTHKSLV  
YLWFLCSSVALALGALTVWHAVLISRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK  
VFLGVD TGRHWLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV

**Important features:****Transmembrane domain:**

amino acids 88-100,202-216,254-274

**N-myristoylation sites:**

amino acids 55-61,56-62,92-98,210-216,309-315,319-325,340-346

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 201-212

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**FIGURE 253**

GATCAAGCGCCTTCCTTTCCCTTCCTCTCCCTACTTGGCCTTTGCCCTAAGCCAAGACCTGGCCATCAGCCTGGC  
TGCAGGGGCGCTGCAGAGCCAGCTGCACTTTTTTCAGGTATGGGGGAGGGCCAGGCACCAATGAAGCCAGTGTGGGT  
GCCACCCTTCTGTGGATGCTACTGCTGGTGCCAGGCTGGGGGCCGCCGGAAGGGGTCCCCAGAAGAGGCCTCC  
TTCTACTATGGAACCTTCCCTCTTGGCTTCTCCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG  
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTCTTCACACACAGTGGGAAGGGGAAAGTGCTTGGGAATGAG  
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATTCTGCTGAGGGAAGTGCACGTCAAC  
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCCTGCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA  
ATCGAATTCTACAGTGATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGCACCACTGG  
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTCAGAGACTAC  
GCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGGATCACGTTCACTGATCCTCGGGCAATGGCA  
GAAAAAGGCTATGAGACGGGCCACCATGCGCCGGGCCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACAC  
CACATCATTAAGGCCACGCCAAAACCTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG  
GGAATTTCACTGAACTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA  
TACCTACAGTTCTGTCTGGGCTGGTTTGCCAACCCCATTTATGCCGGTGACTACCCCAAGTCATGAAGGACTAC  
ATTGGAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC  
ATTAAAGGCACATCCGATTTCTTGGGATTAGGTCAATTTTACTACTCGGTACATCACGGAAAGGAACTACCCCTCC  
CGCCAGGGGCCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTTGACCCAACTGGCCAGATCTGGGGTCT  
AAATGGCTATATTCTGTGCCATGGGGATTTAGGAGGCTCCTTAACCTTTGCTCAGACTCAATACGGTGATCCTCCC  
ATATATGTGATGGAAAATGGAGCATCTCAAAAATCCACTGTACTCAATTATGTGATGAGTGGAGAATTCAATAC  
CTTAAAGGATACATAAATGAAATGCTAAAAGCTATAAAAGATGGTGCTAATATAAAGGGGTATACTTCCTGGTCT  
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA  
AATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGGTTTCCCAATCCA  
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTTGGAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT  
TTGCTAAGTCACATGCAAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGTCTCATCACTGCT  
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTAGAGACAGGATTATCAATTTTGGAGCTTCATAAGAGAATCTT  
CAGGATCTTCCTCCCTTTTCTGCTTTGAGGGTTTCCATACATTGCTGTTTTTCAAGTTCTACAATAATTACCTTTT  
TTTCTCTTCTCTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAATAAAAATAAGCAGAAATTA

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**FIGURE 254**

MKPVWVATLLWMLLLVPRLGAARKGSPEEASFYYGTFPLGFSWVGSSAYQTEGAWDQDGKPSIWDVFTHSGKG  
KVLGNETADVACDGYKQVEDIILLRELHVNHYRFSLSWPRLPTGIRAEQVNKKGIEFYSDLIDALLSSNITPI  
VTLHHWDLPQLLQVKYGGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEKGYETGHHAPGLKLRGTG  
LYKAAHHIIKAHAKTWSYNTTWRSKQQGLVGISLNCWDGEPVDISNPKDLEAAERYLQFCLGWFFANPIYAGDYP  
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGPSYQNDRLIELVDPN  
WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPPYYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK  
GYTSWSLLDKFEWEKGYSDRYGFYYVEFNDNRNKPYPKASVQYYKKIIIANGFPNPREVESWYLKALETCSINNQ  
MLAAEPLLSHMQMVTEIVVPTVCSLCVLITAVLLMLLLRRQS

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 541-558

**N-glycosylation sites:**

amino acids 80-84,171-175,245-249

**Glycosaminoglycan attachment site:**

amino acids 72-76

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 23-27,564-568

**Tyrosine kinase phosphorylation sites:**

amino acids 203-211,347-355,460-468,507-514

**N-myristoylation sites:**

amino acids 44-50,79-85,167-173,225-231,257-263,315-321

**Amidation site:**

amino acids 307-311

**Glycosyl hydrolases family 1 active site:**

amino acids 407-416

**Glycosyl hydrolases family 1 N-terminal signature:**

amino acids 41-56

**Motif name Glycosyl hydrolases family:**

amino acids 37- 67



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**FIGURE 255**

CGCGAAGATGCGAAAGGTGGTTTTTGATCACCGGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG  
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA  
GGCAGAAGCTGTCTGTGCTGCTCTGCTGGCCTCTACCCCACTGCTGAGGTCACCATTGTCCA  
GGTGGATGTCAGCAACCTGCAGTCGGTCTTCCGGGCCTCCAAGGAACTTAAGCAAAGGTTTCA  
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAATAAATATCAAAGC  
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTTCATATGTTCTCCACAGCTGAAGGCCTGCT  
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG  
CCATTTTATCCTGATTCGGGAACCTGGAGCCTCTCCTCTGTACAGTGACAATCCATCTCAGCT  
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTAGCCTCGAGGACTTCCAGCACAG  
CAAAGGCAAGGAACCTACAGCTCTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA  
CAGGAACCTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA  
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT  
TCGCTTTTTTGCAAATGCATTCACCTTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT  
TTTCCACCAAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCTT  
TGGAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA  
TCAAAAGTTACTGGAACCTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC  
CAGGCTCAGTGGCTCATGCCTATTAATTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT  
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGCTCTACAAAAAGAAAT  
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG  
GGAGGATCTCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC  
AGCCTGGGTGACAGCGAGACCCTGTCTCAAAATATGTATATATTTAATATATATATAAAACCA  
GAGCTGACAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTTC  
TACTGAGTTGGATAATATGCATTTGTAATAAACTATGAACTATGAA

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**FIGURE 256**

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD  
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ  
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFQHSGK  
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLLMPAILLLRF  
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAEKFYQK  
LLELEKHIRVTIQKTDNQARLSGSCL

**Important features:****Transmembrane domain:**

amino acids 234-254

**N-glycosylation sites:**

amino acids 37-41,178-182,229-233,263-267

**Glycosaminoglycan attachment site:**

amino acids 12-16

**N-myristoylation sites:**

amino acids 9-15,13-19,15-21,215-221,224-230

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**FIGURE 257**

CGGACGCGTG GGGCCGT **ATG**CGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC  
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC  
ATATACGGGCAGTGGGCACCAATTCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCCTGAGCCCGATGGGGGCTGATGGTGCTCCCTAAGGACAGCATTCAGTTTTCTTCTG  
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTTGGGAAGACCATATCCTCCATACTCCTTGCCGATTTCTCTTGGAACAACATCACTGATT  
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA  
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT  
GCCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG  
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC  
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG  
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG  
CCTTCAATCTGACGTTGCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCTCCACTAGTCCTGGGCA  
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGTTCTGCTGC  
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAAT **TAA**GGCCCCGCTCTCTGGAGGGAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC  
GGCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG  
GGCTATTGATAAGGTCCCCTTGGTGTGCTTCTTGCACTCTCCACACATTTCCCTTGGATGGG  
ACTTGCAAGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTTTCACAGGGAAAAAAAAAAAA

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**FIGURE 258**

MRGSVECTWGWGHCAPSPLLLWTLALLFAAPFGLLGKTRQVSLEVIPNWLGPLQNLLHIRAVG  
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS  
LAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLEFGLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGSPLPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPLVLGIMAVAL  
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

**Important features:****Signal peptide:**

amino acids 1-35

**Transmembrane domain:**

amino acids 365-386

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern:**

amino acids 371-393

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**FIGURE 259**

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCCT  
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTGCGCTCTGTTTG  
GGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAACATAAAATTGAAAGCAAGATTGAAGAGATGGT  
TGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTTTATC  
AGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTTCGTGGGCTCCCATCTAACTGACAACTCAT  
GATGGACGGCCACGAGGTGACCGTGGTGGACAATTTCTTCACGGGCAGGAAGAGAAACGTGGAGCACTGGATCGG  
ACATGAGAACTTCGAGTTGATTAAACCACGACGTGGTGGAGCCCCCTCTACATCGAGGTTGACCAGATATACCATCT  
GGCATCTCCAGCCTCCCTCCAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATTGGGACATT  
AAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC  
TGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG  
CAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAGTGCGAGTGGCCAGAATCTT  
CAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCAGGCGCTCCAGGG  
GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCCAGTACGTCAGCGATCTAGTGAATGGCCT  
CGTGGCTCTCATGAACAGCAACGTCAGCAGCCCGGTCAACCTGGGGAACCCAGAAGAACACACAATCCTAGAATT  
TGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA  
GAAAAGAAAACCAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGCTCCCGCTGGAGGAAGGTTT  
AAACAAAGCAATTCCTACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC  
TGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTGAACTCCTCACTTTTAGGACACAAGACTACCATTGTACAC  
TTGATGGGATGTATTTTGGCTTTTTTTTGTGTGCTTTAAAGAAAGACTTTAACAGGTGTCATGAAGAACAAC  
TGGAATTTCACTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAGCTCCCTCAAAAACTGCAGATTTTG  
CCTTGCACTTTTGAATCTCTCTTTTTATGTAAATAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTTAT  
CTTGCTGTGAGAGCATATGTTGTGACTGTCGTTGACAGTTTTATTTACTGGTTTCTTGTGAAGCTGAAAAGGAA  
CATTAAGCGGGACAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT  
AAAGAAAAATCCTAGCAGTATTGTCAGGTGGTGGTGCGCCGGCATTGATTTTAGGGCAGATAAAAGAATTCTGTG  
TGAGAGCTTTATGTTTCTCTTTTAATTCAGAGTTTTTCCAAGGTCTACTTTTGAGTTGCAAACTTGACTTTGAAA  
TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTTGCTGCGTATCTGGGGCGGGGGCAGGT  
TGGGGGGCACAAAGTTAACATATTCTTGGTAAACCATGGTTAAATATGCTATTTTAATAAAATATTGAACTCA

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**FIGURE 260**

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR  
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVDNFFTGRK  
RNVEHWIGHENFELINHADVVEPLYIEVDQIYHLASPPNYMYPNPIKTLKTNLTIGTLNMLGL  
AKRVGARLLLASTSEVYGDPEVHPQSEDYWGHVNPIGPRACYDEGKRVAETMCYAYMKQEGVE  
VRVARIFNTFGPRMHMNDGRVVSNFILQALQGEPLTVYSGSQTRAFQYVSDLVNLGLVALMNS  
NVSSPVNLGNPEEHTILEFAQLIKNLVSGSGSEIQFLSEAQDDPQKRKPDIKKAKMLGWEPVV  
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

**Important features:****Signal peptide:**

amino acids 1-32

**N-glycosylation site:**

amino acids 316-320

**Tyrosine kinase phosphorylation site:**

amino acids 235-244

**N-myristoylation sites:**

amino acids 35-41, 101-107, 383-389

**Amidation sites:**

amino acids 123-127, 233-237

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**FIGURE 261**

GCGTGGTGCGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG  
CATCCTCCGCATCCTCCACATCCTTCCATGGGCTCTGAAGAATAAATTCAGTTGTTTATGGATC  
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT  
ATAGACAACTGCATAGAAGCCCAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGAC  
ATGAAATACATGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAGTGC  
AAATTTGAACATAATGACTGTTTGGATAAATCATATAAATGCTATGCAGCTTTTGAATATGTT  
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGG  
TATAATGAAACCCAATTTTATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT  
ACACAGTTAGTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTT  
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAATATG  
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAAC  
CTCTGCAGGACTCCACAACCTTATTATACCTAACCAAAATCCATTTCTGAAGCCAACGGGGAGA  
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTTTAA  
TGTCATTTATATACAAAAGAAATTCTCAAATGTTAAAATAAAGGAATAGTTTATTGCTTAATA

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**FIGURE 262**

MALKNKFSCWLWILGLCLVATTSSKIPSITDPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG  
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF  
DSLSCSRVCGHYTQLVWANSFYVGCAVAMCPNLGGASTAIFVCNYGPAGNFANMPPYARGESC  
SLCSKEEKCVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGFLLLRIF

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site:**

amino acids 119-123

**N-myristoylation sites:**

amino acids 103-109,150-156,160-166,161-167,175-181

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:**

amino acids 136-156

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

amino acids 166-178



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**FIGURE 263**

CGCCCTCCGACCCGCCCCGCGGCGCATTGTGGGATCTGTGGCTTGTCAGGTGGTGGAGGAAA  
AGGCGCTCCGTCAATGGGGATCCAGACGAGCCCCGTCCTGCTGGCCTCCCTGGGGGTGGGGCTG  
GTCACCTCTGCTCGGCCTGGCTGTGGGCTCCTACTTGGTTCGGAGGTCCCGCCGGCCTCAGGTC  
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC  
AACACCAAGAGGTTCCGCTTTGCCCTGCCACCGCCCACCACACTCTGGGGCTGCCTGTGGGC  
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTC  
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTCAATCAAGGTCTACCTGAAGGGTGTGCAC  
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTTGGGGATGTG  
GTGGAGTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAACATTTCAG  
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG  
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC  
CAGTGCTTTCTGCTTTTGTGCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG  
GAACTGCAGGCCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCCTCTGGATCATCCCCAAAA  
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCCGCTCCA  
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCAATGGTGCAGCTGGCCTGCCATCCC  
AACTTGACAACTGGGCTACTCACAAAAGATGCGATTACCTACTTGAGCATCCTCCAGCTTC  
CCTGGTGCTGTTTCGCTGCAGTTGTTCCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCCCT  
TTCCTCAGAGTTTCAGGTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG  
AACAAATATTCCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA  
TCTCCCCGTGGCAACAGGTCCAGGAGAGGCCCATGGAGCAGTCTCTTCCATGGAGTAAGAAGG  
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCTTGATAGCATCTTACTCTCACCTT  
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAACTTCACTGTTCAA  
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT  
ATGGAGATGGCAAGAAAGGAGGAAATGATTTCTTCAGATNTCAAAGGAGTCTGAAATATCATA  
TTTCTGTGTGTGTCTCTCTCAGCCCCCTGCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA  
AACTGCTGTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA  
TATTGAAGA

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**FIGURE 264**

MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTR  
FRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP  
EGGKMSQYLDLKVGDVVEFRGPSGLLTGTGKGFNIQPNKKSPPPEPRVAKKLGMIAGGTGIT  
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLWFTLDHPPKDWAY  
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

**Important features:****Signal peptide:**

amino acids 1-26

**N-glycosylation site:**

amino acids 214-218

**N-myristoylation sites:**

amino acids 22-28,76-82,128-134,180-186

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**FIGURE 265**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA  
ACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAG  
AATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTCGGT  
TCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGGATGTTGGGGGCCCCGCCTCAGG  
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC  
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC  
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC  
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGA  
AGATACCTCTGCATGGATTTTCTCAGAGGCAACATTTTTGGATCACACTATTTGACCCGGAGAAC  
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC  
TTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTAC  
TCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACCCCCATACCACGG  
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGG  
GCCCCGATGACCCCGGCCCCGGCCTCCTGTTTACAGGAGCTCCCGAGCGCCGAGGACAACAGC  
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAACACGCACGCTGGGGGA  
ACGGGCCCCGGAAGGCTGCCGCCCCCTTCGCCAAGTTCATCTAGGGTTCGCTGG

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**FIGURE 266**

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNHVDG  
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDV  
YHSPQYHFLVSLGRAKRAFLPGMNPPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSERDP  
LNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFAKFI

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

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**FIGURE 267**

GGCTGAGGGGAGGCCCCGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC  
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC  
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG  
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG  
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACT  
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG  
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGCAAGGACCATGAGG  
CCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTT  
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGAC  
AAGTGCACCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG  
GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG  
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC  
CGCAACATGAACTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCG  
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG  
GACCTGGAGCACAAAGTACCAGCACCTGGCCCACTGGCCCCACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG  
CACTGCCAGAGGGTGCCCTCGGCCAGGCCCCGTCCCCAGCCACCCCCCGCTGCCCCGCCCCGGGTCTACCAACCA  
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA  
CCCCCTCTGCCCCACTATGCCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGGCCCATGGAGAGAC  
TGCCTGCAGGCCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTC  
ATGCAGGTGTGGTGCAGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATGGCTCTGTT  
AACTTCTTCAGGAACCTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG  
AACATTTACTGGCTGACGAACCAAGGCAACTACAAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC  
TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC  
AATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTTACCACCCTGGACAGAGATCATGATGTCTACACA  
GGAAACTGTGCCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGG  
TACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTTAAGCCAGCTCCCCCTCCTGACCTCTC  
GTGGCCATTGCCAGGAGCCACCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTACCAGTTCATCCTGA  
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGATACGGT  
GTTTTCTGTCCCTCCTACTTTCTTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA  
CTCTTTCTTTAAATAAATAAAGTCTCTACAATAAAAAAA

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**FIGURE 268**

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ  
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLRKE  
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQADMLQLASKYKDLEHKYQHLATL  
AHNQSEIIAQLEEHQQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLV  
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGG  
WTVIQRRLDGSVNFFRNWETYKQGGFNIDGEYWLGLENIYWLTNQGNKLLVTMEDWSGRKVF  
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYQKGGWWYN  
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH

**Important features:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites:**

amino acids 164-168, 192-196

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 124-128

**Tyrosine kinase phosphorylation sites:**

amino acids 177-184, 385-393, 385-394, 461-468

**N-myristoylation sites:**amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,  
473-479**Amidation site:**

amino acids 373-377

**Fibrinogen beta and gamma chains C-terminal domain signature:**

amino acids 438-451

**Fibrinogen beta and gamma chains C-terminal domain proteins:**

amino acids 305-343, 365-402, 411-424, 428-458

**Trehalase proteins:**

amino acids 275-292

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**FIGURE 269**

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA  
GCGGGTCTTACCCCCGGTCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGA  
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC  
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC  
CAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCTGGCGCACGGACTCCTGCAGCT  
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCG  
CCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC  
TGAGAGCCGGGTGGACCCTGAGGTCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG  
CAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTGGAGAAGCAGCACCT  
GCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT  
GGCCAAGCCTGCCCCGAAGAAAGAGGCTGCCCCGAGATGGCCCAGCCAGTTGACCCGGCTCACAA  
TGTCAGCCGCCTGCACCGGCTGCCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA  
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTTGGTGAACCTGCAAGATGAC  
CTCAGATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC  
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA  
GGTGCATAGCATCACGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGG  
CAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCA  
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT  
ACCCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCT  
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC  
CATCCACAGCAGCGGCAGAAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCGCTA  
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTTAGCG  
TCCTGGCTGGGCCTGGTCCCAGGCCACGAAAGACGGTGACTCTTGGCTCTGCCCCAGGATGT  
GGCCGTTCCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAAACTTGTGGACAGAGAA  
GAAGACCACGACTGGAGAAGCCCCCTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCTCCTGA  
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGACCAAGGGGCATGGAGCTTCACT  
CCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTTGGGGCCAGCCAGACTGGCCTCAA  
TGGCGGACTCAGTCACATTGACTGACGGGGACAGGGCTTGTGTGGGTGAGAGCGCCCTCAT  
GGTGCTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC  
GGAGCTCACAGAGTTCTTGAATAAAAAGCAACCTCAGAACAC

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**FIGURE 270**

MTVIRFFPAASATKRVLPPVLRVSSPRTWNPNVPESPRIPAPRLPKRMSGAPTAGAALMLCAA  
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA  
CQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS  
QFGLLDHKKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRHLRPRDCQELFQVGERQSGLFEIQ  
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDENRPWEAYKAGFGDPHGEFWLGLEKVHSITGD  
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQ  
DHDLRDKNCAKSLSGGWVFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATT  
MLIQPMAAEAAS

**Important features:****Signal peptide:**

Amino acids 1-13

**Transmembrane domain:**

Amino acids 53-70

**N-glycosylation site:**

Amino acids 224-228

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 46-50;118-122

**N-myristoylation sites:**

Amino acids 50-56;129-135;341-347;357-363

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 396-409



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**FIGURE 271**

CGGACGCGTG GGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG  
AACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAAGCTGGGGCTCCCGCCGCTG  
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTTGACTCG  
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTAC  
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT  
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGCT  
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAACT  
CTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG  
ACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCAGTCTAAGCCAGAAATCCAG  
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC  
TATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC  
TTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCTTGTCTCTCGGTG  
ATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT  
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA  
GCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT  
ACAAAAGTGAATCTTGCTCATTCTGAAATTTTAAGCATTTTTCTTTTAAAGACAAGTGTAATA  
GACATCTAAAATTCCACTCCTCATAGAGCTTTTAAATGGTTTCATTGGATATAGGCCTTAAG  
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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**FIGURE 272**

MAAPKGSLWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYPK  
EEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL  
RQEQLMSLMPKMHLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEIQYA  
PHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVLSVMV  
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAGPLPTK  
VNLAHSEI

**Important features:****Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site:**

amino acids 90-94

**N-myristoylation sites:**

amino acids 28-34,29-35,31-37,86-92

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**FIGURE 273**

CCCACGCGTCCGAACCTCTCCAGCGGATGGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGTG  
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA  
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT  
GCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCAT  
AGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT  
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTT  
CACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGGGCTGGTT  
CATGGCCTTCACGCGGCAGGGGCGGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA  
GGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGCCGAGAAGCA  
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGGACCAAGCGCACACGGCGGGCCCCA  
GCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCCCACCCCTTTCC  
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC  
TGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC  
TGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTCACCCTGA  
TCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGC  
GACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCTCAAATCTGCTTCTCGGATCT  
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGT  
GTTTGTGTTGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAGAGGGTTGTCCACTCCTCA  
CATTCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCCCGGAATAAAACCATTTTCC  
TGC

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**FIGURE 274**

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHHVQVTGRRIS  
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLENN  
YTAFQONARHEGWFMFAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEEKQKQFEFVGS  
APTRRTKRTRRPQPLT

**Important features:****Signal peptide:**

Amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

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**FIGURE 275**

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT  
TTTTATTCTCTGTCCTATTTGCCATCTCAGAAAGTGC GGAGCAAGGAGTCTGTGAGACTCTGTG  
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG  
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAAACTCCTTCCAGCTCCCACATAAACGTG  
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC  
TTTGGGGTGGACAGATGCCCCTGAAGAGCTTTGGAAGTCAAAGAAGCATTTCAGTGATGTCAA  
GACAAGATTTACAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT  
GCTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT  
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAAATGATGGCTTTTGGGTAGGCAAACT  
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC  
AAGGTTAATGAACTGTTCTTTTCAAATTCTACTAATGCTTTGAAATTTCAAATGCTGCGCAAA  
ATTGCAATAAAAATGCTATAAA

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## **FIGURE 276**

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGN  
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKS KHSVMSRQDLQTL CCTDGC  
SMTDLSALC

**Important features:**

**Signal sequence:**

amino acids 1-18

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 107-111

**N-myristoylation sites:**

amino acids 3-9, 52-58, 96-102, 125-131

**Insulin family signature:**

amino acids 121-136

**Insulin family proteins:**

amino acids 28-46

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**FIGURE 277**

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTCTCTGCTGGATTAAAGACGG  
CCCACAGACCAGAACTTCCACTATACTACTTAAAATTACATAGGTGGCTTGTCAAATTCAATTGATTAGTATTGT  
AAAAGGAAAAAGAAGTTCCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCT  
CAGATGAACAACTTCTACACTGATTTTTAAATCAAGAATAAGGGCAGCAAGTTCTGGATTCACTGAATCAAC  
AGACACAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAACCAACGCATAGAAGAC  
TTTTTTTTCTCTTCTAAAAACAATAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAAT  
GAAGACTTTTACCTGGACCCTAGGTGTGCTATTCTTCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT  
CAAAATTAATAAAATAAACAGAGAAGATACCCTCGTGCCACAGATGGTAAAGAGGAAGCAAGAAATGTGCATA  
CACATTCTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT  
TAAAGACATGATCACCAGGATGGACCTTGAAGACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGT  
TCTGCAACTGGTGGTGGATGTAGATGGAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACAT  
GAACCTCTCGTGTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCATTGAACT  
TTCCCAACTGGAAAACAAAATCCTCAATGTCAACACAGAAATGTTGAAGATGGCAACAAGATACAGGGAACTAGA  
GGTGAATACGCTTCCTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTT  
GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCCCACTTGTCCAGGTGGTGCCACAACATATTCCTAACAG  
CCAACAGTATACTCCTGGTCTGCTGGGAGGTAAACAGATTCCAGAGGGATCCAGGTTATCCCAGAGATTTAATGCC  
ACCACCTGATCTGGCAACTTCTCCCACCAAAAGCCCTTCAAGATACCACCGGTAACCTTTCATCAATGAAGGACC  
ATTCAAAGACTGTCAAGCAAGCAAAAGAAGCTGGGCATTCCGGTCAGTGGGATTATATGATTAAACCTGAAAACAG  
CAATGGACCAATGCAGTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTGGACTGTTATTTCAGAAAAGAACAGA  
CGGCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT  
TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGA  
TAAAAAAGTCTATGCAGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAAC  
TTACCAGGGAAATGCAGGGGATTCTATGATGTGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGA  
TATGTATGCAGGAACTGCGCCCACTTTCATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAA  
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCACCAAGATGGAATTTTCTGGGCCGAATACAGAGGCGG  
GTCATACTCCTTAAGAGCAGTTTCAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTAAATGA  
CACAGAACTTTGTACTTTTCAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTAC  
ACAGAAAGTTTTTAAATGAATTTTACCCTAACTATAAAAGGGAACCTATAAATGTAGTTTTCATCTGTCGTCAT  
TACTGCAGAAAATTATGTGTATCCACAACCTAGTTATTTTAAAAATTATGTTGACTAAATACAAAGTTTGTTTTCT  
TAAATGTAAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA  
CTTAACAATTTATTTAAATCTAAGATTGCTCTAACGTCTAGTGAAAAAATATTTTTTAAATTTTCAGCCAAATA  
ATGCATTTTATTTTATAAAATACAGACAGAAAATTAGGGAGAACTTCTAGTTTGGCAATAGAAAATGTTCTT  
CCATTGAATAAAAGTTATTTCAAATTGAATTTGTGCCTTTCACACGTAATGATTAAATCTGAATTCCTAATAATA  
TATCCTATGCTGATTTTCCCAAAACATGACCCATAGTATTAATACATATCATTTTAAAAATAAAAAAAACCC  
AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAAGACAAATCTATGAATGAATTTTTCAGTGTATCTT  
CATATGATATGCTGAACACCAAAATCTCCAGAAATGCATTTTATGTAGTTCTAAAAATCAGCAAAATATTGGTATT  
ACAAAAATGCAGAATATTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTATTACTTTTTTTCTAATTT  
ACTGATCTTACTACTACAAAGAAAAAAACCAACCCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC  
AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAAACAACTCAAGGAACCTGTTGGCTGTTTTCCCGATACTGA  
GAATTCAACAGCTCCAGAGCAGAAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTTCAATTTTACAGTGTAT  
GTAACGCTTAGTCTCAGAGTGTCTTAACTCATCTTTGCAATCAACAACCTTACTAGTGACTTTCTGGAACAATT  
TCCTTTTCAGGAATACATATTCACTGCTTAGAGGTGACCTTGCTTAATATATTTGTGAAGTTAAAATTTTAAAGA  
TAGCTCATGAACTTTTGTCTAAGCAAAAAGAAAACCTCGAATTGAATGTGTGAGGCAACTATGCATGGGAAT  
AGCTTAATGTGAAGATAATCATTTGGACAACCTCAAATCCATCAACATGACCAATGTTTTTCATCTGCCACATCTC  
AAAAATAAATCTCTGGTGAAACAAATTAACAAAAATATCCAAACCTCAAAAAAA

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**FIGURE 278**

MKTFTWTLGVLFLLVDTGHCRRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP  
ICVNTKGQDASTIKDMITRMDLENLKDVLRSRQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM  
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQ  
SVMITLLEEQLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGNEIQRDPGYPRDLMP  
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP  
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWSDKK  
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGWW  
YNACAHSNLNGVWYRGGHYRSKHQDGI FWA EYRGGSYSLRAVQMMIKPID

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation sites:**

Amino acids 160-164;188-192

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 120-124

**Tyrosine kinase phosphorylation sites:**

Amino acids 173-180;387-396

**N-myristoylation sites:**Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;  
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453



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**FIGURE 279**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGGC  
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGCCG  
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAAGCC  
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGGCAAGTCGCGAGACAGCGGACAAGCAGCGGA  
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGGCGTCG  
TGGCCATGGCGGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCGAGCGCG  
AGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA  
ACAAGTTAAATGTCTTTTCCCGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAGAAGAAGAC  
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAGC  
TGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTTAACC  
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA  
TGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCAAATTCAAAGAAT  
CAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAGCAGCAGTCAGGCC  
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA  
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC  
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT  
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA  
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA  
CCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGGCAGAGTTCACTATTCTATC  
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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**FIGURE 280**

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKRRRRRPE  
PQLKGIVTKLYSRQGYHLQLQADGTIDGTDKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLAMN  
SEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLNKEGEIMKGNHVKKNK  
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

**Important Features:****N-glycosylation site:**

Amino acids 242-246

**Glycosaminoglycan attachment sites:**

Amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site:**

Amino acids 93-100

**N-myristoylation sites:**

Amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 231-239

**HBGF/FGF family proteins:**

Amino acids 78-94, 102-153

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**FIGURE 281**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA  
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA  
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCTCCA  
TTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTCCTGACATTGGCAGTGCCCC  
AGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG  
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAAACCACG  
TCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA  
GGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA  
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG  
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCCTGTGGGTGGGGCAGCGAGTCGGGG  
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG  
CGCCTGCCGTTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGGCGCTGGCCAGTAGCCTGAT  
CCGGCAGAAGCGGGAGGTCCGCGAGCCCCGGGGCAGCCGGCCGGTGTGCGCGCAGCGGCGCGT  
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG  
ACTGTGCGGGGGGGCGGCCCCGCGCGGCCGGACCGCGGCCCGGAGCCTCAGCTCAAAGGCATCGT  
CACCAAATGTTCTGCCGCCAGGGTTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG  
CACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT  
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG  
TTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT  
GTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCCTGGTACCTCGGCCTGGACAA  
GGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCCACTTTCTGCC  
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC  
TTCCAGTCCCCCTGCCCCCTGAAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA  
GCCAGCCACCACCAACCTGT

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## **FIGURE 282**

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDRG  
PEPQLKGIIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHYMA  
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK  
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

**Important features:**

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 54-60; 89-95; 131-137

**HBGF/FGF family signature:**

Amino acids 131-155

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**FIGURE 283**

**ATG**CCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG  
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACGGC  
AACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC  
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA  
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC  
CTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAACAGGGTTGTATATAGCC  
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA  
TCTGTTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT  
AGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA  
ACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT  
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAAGTGCG  
TCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACAT**AG**

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**FIGURE 284**

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLRR  
QDPQLKGIVTRLYCRQGYLQMHDPDGDGTDKDDSTNSTLFNLI PVGLRVVAIQGVKTGLYIA  
MNGEGYLYPSELFTEPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK  
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

**Important features:****N-glycosylation sites:**

Amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins:**

Amino acids 104-155, 171-198

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**FIGURE 285**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCAGGTTTTGCTTTGA  
TCCTTTTCAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCTT  
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAC  
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC  
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
GAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
TCTGCATCCACTACAACATTGTCTATGCCACAATTACAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG  
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTTGTTTTGGAA  
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT  
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
GTGGGAAGTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA  
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT  
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA  
ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAGAAATTAATGTTGTAT  
TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTAGTTCTTTC  
GATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC  
TCTAAAGCTCCATGTCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTCACAT  
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAAGTATGTTGCTATGAATTAAGTTGT  
GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATTTCTGCCATTTAGAAGAAGAGAACTACA  
TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG  
TTTCATTGTGTACATTTTATATTTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCT  
ATTTTTACCAAAGGTATTTAATATTCTTTTTATGACAACTTAGATCAACTATTTTGTAGCTGGTAAATTTTTCT  
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
TTCTCGTATGGTGTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA  
GACTTTTTGAAAATAATTAAATTATCATATCTTCCATCTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA  
AAGTAGACATTAGATCCAGCCATTACTAACCTATCTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA  
TTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA  
GAAGTATGTCTCTTAACAGTTCACTTATTGTACTCTGCCAATTTAAAAGAAAATCAGTAAAATATTTTGTCTGT  
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGA  
ATGTGGCTATTTTGGGGAGAAAATTAATAAAAAAAAAAAAAAAAAAAGGTTAGGGATAACAGGGTAATGCGGCC

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**FIGURE 286**

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF  
PHTYPRNTVLVWRLVAVEENVWQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS  
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNA  
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGAFVFGRKSRVVDLNLLEEVRLYSCTP  
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKT  
GVRGLHKS LTDVALEHHEECDCVCRGSTGG

**Important features:****signal sequence:**

Amino acids 1-14

**N-glycosylation sites:**

Amino acids 25-29;55-59;254-258

**N-myristoylation sites:**

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

**Amidation site:**

Amino acids 229-233



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**FIGURE 287**

CAGCGCTGACTGCGCCGCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC  
CGCTCGGCCTGGCCAGGCCCGCGCT**ATG**GAGTTCCTCTGGGCCCCTCTCTTGGGTCTGTGCT  
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA  
ATGAGGACTACACCATAACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG  
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG  
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG  
CCAAGCATGGCCCGGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTCACCCCTGGGCA  
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC  
GCTGCTTGAGGTTGAAGGTGACTGTCAGTGGCAAAATCACTCACAGTCCTCAGGCCCATGACA  
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC  
ACAGTGCTGCCCCACGCCTCTTCCCACTTGCCCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC  
TGCAAACCCCG**TGA**AGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA  
CAGGCACTCCAAACCTGTCTTGGGGCCACTTTCAGAGCCCCAGCCCTGGGAACCACTCCAC  
CACAGGCATAAGCTATCACCTAGCAGCCTCAAACGGGTCAATATTAAGGTTTTCAACCGGAA  
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG  
GAGACAGTCCTTTCCCACCATTCCTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC  
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA  
TGCCCCCTTCAGGAGAGAGCCAGGATGCCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG  
TTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCAG  
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTTGTAGCCAGGTACTGCATTCTCTCCCAT  
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG  
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC  
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCCTGATTTCTACAACCTGGAGTTTT  
TTTATACAATGTTCTTTGTCTCAAATAAAGCAATGTGTTTTTTTCGG

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## **FIGURE 288**

MEFLWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM  
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGHSYY  
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHDNPQEKRLAADDPEVRVLHSIGHSAAPRLFPL  
AWTVLLLPLLLLQTP

**Important features:**

**Signal sequence:**

Amino acids 1-17

**N-glycosylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 118-127

**N-myristoylation site:**

Amino acids 10-16

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**FIGURE 289**

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTTC  
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGGG  
CTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGGCTC  
CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCTCAGCCCCATCCGTGTCATACCTGCCGG  
GGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAGGTGGA  
AACACTGCCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG  
GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG  
GAGCTGGTGGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCCGGACCTCTTCCAGTGGCTG  
TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCCTGCCTTCCCTGT  
CCTGGGGGAACAGAGAGGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGGGACACGAGGG  
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT  
GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGT  
GCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGGCTGGGCCCTGCAT  
CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACCTGTGGAGCTGACCAA  
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC  
ATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAG  
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAACAAGCAGTGTGAAAAC  
ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG  
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG  
CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC  
TTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTGAGAG  
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATAATCGCGGCCACCACCTGTAGGA  
CCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC  
TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCCAGGTACCC  
AGGCCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT  
TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAGTTTTTCCTTAATGGTG  
GCTGCTAGAGCTTTGGCCCCTGCTTAGGATTAGGTGGTCCTCACAGGGGTGGGGCCATCACAG  
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCCACATCCCCACACCCCA  
TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGGAAGTTAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT  
IRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE  
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAGYGG  
EACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDECSTE  
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCP  
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTDELVLVLMFFGIICAL  
ATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Important features:****Signal sequence:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 342-392

**N-glycosylation sites:**

Amino acids 79-83;205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 290-294

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 321-333

**EGF-like domain cysteine pattern signature:**

Amino acids 181-193

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**FIGURE 291**

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC  
GCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTGGAAGGAGGGAGTGCGCGGGCTGCCCC  
GGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTTCCAGGCACCCTGTCTGGGGCAGGGAGGGGCACAGGCCTGC  
ACATCGAAGGTGGGGTGGGACCAGGCTGCCCCCTGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCGTGGCCCTG  
CAGACTCTCAGGGCTAAGGTCCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGTAGC  
TTGAAGGAGGCACCATGTCAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCTGGCTCAGGCCTGCCCTG  
AGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC  
CTGGCTTCCCGCCAATGTGACTACACTGAGCCTGTGAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCA  
GGGAGGTGCCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCT  
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTCCTGGAGCGACCTGCACAACC  
TCAGTGGCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGGACGCCTTCCGCAGCCTCC  
GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACATTGGCCGAGGGCACCTTACCCCCGCTACCCG  
CGCTGTCCACCTGCAGATCAACGAGAACCCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCC  
TGACCACGGCCGTGTCCATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGC  
TGAGCCGCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGGC  
AGCTGCGGCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGAGCCGGCCCTCAGCTTCACTGGCACA  
TCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAACGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCC  
CTGTGGCCAGCTCCAGCCGCGCTTCCAGGCCTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGG  
AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCCA  
CGCCCGGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAAAGGGCTGCTATA  
CGGTTGACAACGAGGTGCAGCCATCAGGGCCGAGGACAATGTGGTCATCATCTACCTCAGCCGTGCTGGGAACC  
CTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCGAGCTGCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCC  
TCTTCTTCTCCTCACCTCCTTCTAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCCACCAATGCCCC  
TTTAAGTGCTGCAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCTCC  
TTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAACTAGTGACTAGGATAGAATTTG  
ATCCCCTAACCTACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTGCCTGTGCTCTCCTCTCAGGGGCAGCATG  
CTAACGGGGCGACGTCTAATCCAACCTGGGAGAAGCCTCAGTGGTGGAATTCAGGCACTGTGACTGTCAAGCTG  
GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAG  
GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCTCCTTG  
CTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG  
CCTTCCTTCTCTTACCCTTCCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCCTTTCTCCCCAACT  
ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATG  
CCAAAAAAGGGCGCCGCGACTCTAGAGTCGACCT

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**FIGURE 292**

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFPPANVTTLSSLNRLP  
GLPEGAFREVPPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLNLSDFAWSDLHNLSALQL  
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCTCGIV  
WLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELRPGFV  
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLIP  
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP  
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSF

**Important features:****Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 403-418

**N-glycosylation sites:**

Amino acids 51-55, 120-124, 309-313

**Tyrosine kinase phosphorylation site:**

amino acids 319-326

**N-myristoylation sites:**amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,  
350-356, 394-400**Amidation site:**

amino acids 355-359

**Leucine Rich Repeat:**

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

**Leucine rich repeat C-terminal domain:**

amino acids 180-230

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**FIGURE 293**

ACTTGGAGCAAGCGGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC  
TCGCTTCCCAGGCGCCGCGGGCTGCAGCCTTGCCCTCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCT  
CTAGGGGACAGACACGCTCGGACCCACCCGACAGCGGCCCTTCTGGAGAGTTCTGTGAGAACAAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA  
TCTTGCAATTCTTGGACATTGGTCCTGATGTCAACCGAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTGGCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCCTCAGAAAACACGGATGTGAAC  
ATGAGTGTGTAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACCTGCAGCCGAGTGGACCACCTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTTCGTCTGCCAGTGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCCTGTCACTGTCTGAGGGACACGTGCTCCGACGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTGTGAACATTCTGTGTGAAGCAGTGAAGATTCTTTGTGT  
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATAACGTCGAGTGCTTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCCAACACATTTGTGTTA  
ATAATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTAGCTGAGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTGAGGTCTG  
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTGACAATTTCCCCAAAGCCGCTCGAGTGGGGCTGGTCCAGT  
ATTCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACATAAGAGATTGCCTCTGAGCCCAACAAGCATCTCTTCTATGCCGAAGACTTCAGCACAATGG  
ATGAGATAAGTGAATACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACCTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTGCACTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTTGCCACAGAACAAGACAAGATATACACTAATTTGTATAAATTTATCTAGGAAAAAATCCT  
TCAGAATTTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AATTGCTTCTGCCTCATCCTGCCTTAGTGTGAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAATAATTCACCACTTCAG

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**FIGURE 294**

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHHPQTALLESSCENKRADLVFIID  
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSKTFKRKSEVERAVKR  
MRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI  
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF  
CINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDG  
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGEHECVN  
MEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCEGFLINEDLKTC  
SRVDYCLLSDHGCEYSCVNMDRSFACQCPGHHVLRSDGKTC AKLDSCALGDHGCEHSCVSSD  
SFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCKRK  
DVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF  
EVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT  
GLALKHMFERSFTQGEARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA  
IEEELQEIASEPTNKHLYAEDFSTMDSEIKLKKGICEALESDGRQDSPAGELPKTVQQPT  
ESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM  
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation site:**

Amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 115-119; 606-610; 892-896

**N-myristoylation sites:**Amino acids 133-139; 258-264; 299-305; 340-346; 453-459; 494-500;  
639-645; 690-694;  
752-758; 792-798**Amidation sites:**

Amino acids 314-318; 560-564; 601-605

**Aspartic acid and asparagine hydroxylation sites:**Amino acids 253-265; 294-306; 335-347; 376-388; 417-429;  
458-470; 540-552; 581-593



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**FIGURE 295**

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC  
CATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGC  
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAA  
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAA  
GACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCTGGAGGGGCTGTGCGA  
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTG  
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGT  
GTGCTGCTCTCCAGGAACCTACGGTCCC GACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC  
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTTGCCGGTG  
CCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG  
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCCTGAC  
CAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT  
GGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG  
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAA  
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG  
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCCAGGGAGCTA  
CGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC  
TGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGG  
ACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCT  
CCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTCTAACGGTTGATTCTCATTTGTCCC  
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTTTGT  
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAA

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**FIGURE 296**

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDFKNQGMVDTAKKNFGGGNTAWEEK  
TL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LKV  
CCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR  
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANG  
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY  
VCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

**Important features:****Signal peptide:**

Amino acids 1-24

**N-glycosylation sites:**

Amino acids 190-194;251-255

**Glycosaminoglycan attachment sites:**

Amino acids 149-153;155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 303-310

**N-myristoylation sites:**Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;  
252-258;313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

**EGF-like domain cysteine pattern signature:**

Amino acids 166-178

**Leucine zipper pattern:**

Amino acids 94-116

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**FIGURE 297**

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAGAAAGAGGAAG  
ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCATCATGCTGCTATTCTCTGCAAATACTGA  
AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC  
CACCTTCAAAAAGTACATCAATATTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT  
TTGGACAATGCAATTGTGGCACTGGCACTTATTTTCAAGTGAAGAAAACTTTGTGGTTCTATGGCATTATCATTTT  
GACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTGTGGAATCCTTAAGGGC  
CCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACTCCGAATTCATGTGCTACTTGGCCTAGCTA  
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT  
TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCA  
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAGACTTTC  
CAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAATATTAATGTAAAAAAGATGC  
CTCAGCTCCTTTCTGTGTACCTAGAGGAAACAACTTACTGAACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCA  
ACTTACAAGAACTCTATATTAATCACAACCTTGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATC  
TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAG  
AGATTCTGATGATTGGGGAATCCAAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCAATCTTCGCA  
GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTTGGACTGGAAAACCTTAGAAAGCA  
TCTCTTTTACGATAACAGGCTTATTAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAATTTTGG  
ATCTAAATAAAAATCCTATTAATAGAATACGAAGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGA  
TAAATAATATGCCTGAGCTGATTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG  
CTACTAACAACCCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCAAGCTGGAATCACTCATGC  
TGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTGCCAAACCTCAAGGAAATCAGCATA  
ACAGTAACCCCATCAGGTGTGACTGTGTATCCGTTGGATGAACATGAACAAAACCAACATTTCGATTCTGAGC  
CAGATTCACTGTTTTGCGTGGACCCACCTGAATTCAGGTGAGTCTGCGCAAGTGCATTTTCAGGGACATGA  
TGGAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGTTT  
CCTTTCAGTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTTTC  
CTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACTAGATATAAATGGCGTAACTCCCAAGAAG  
GGGGTTTATATACTTGTATAGCACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT  
CTTTTCCACAAGATAACAATGGCTCTTTGAATATTAATAAGAGATATTGAGGCCAATTCAGTTTGGTGTCTT  
GGAAAGCAAGTTCTAAAATCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCATGCTG  
CGCAAAGTGTCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA  
TTTGTATTGATATTCACCACCTATCAGAAAAACAGAAAAAATGTGTAAATGTCACCACCAAGGTTTGCACC  
CTGATCAAAAAGAGTATGAAAAGATAATACCACAACCTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTG  
GTGTGATATGTCTTATCAGCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACT  
TACAGAAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAAAGAAAAA  
GTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTTAAACCACCAAGGAAACCTA  
CTCCAAAATGAAC

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**FIGURE 298**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF  
PARLPANTQILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN  
KLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDALPN  
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVP  
HVALQKVVNLFKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPDLRKIE  
ATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISHSNPIRCDCVIRW  
MNMNKTNIRFMEPDSLFCVDPPEFQGQNVVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVS  
FHCRTAEPPQPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTCIATNLVGA  
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ  
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLN  
ACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS  
LKVKATVIGLPTNMS

**Important features:****Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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**FIGURE 299**

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTT  
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG  
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT  
ACCATGCCCCGGATCCCCAAGACCCTAAAGTTCGTCTGTCATCGTCGCGGTCTCTGCTGCCA  
GTCCTAGCTTACTCTGCCACCACTGCCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA  
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT  
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT  
TCTTGCTTCCCATGTACAGTTTGTAATCAGATCAAAAACATAAAAGTTCCTGCACCATGACC  
AGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACCTCCCAGAGATGTGC  
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT  
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACA  
ATGAACACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG  
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCT  
GAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC  
AGCCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA  
ATTGTGCTTCTGATTGTGTTTGTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG  
AAAGGTTCAAGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT  
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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**FIGURE 300**

MARI PKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVA PQQRHSFKGEECPAGSHRSEHT  
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCR  
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT  
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLI  
VLLIVFV

**Important features:****Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 240-259

**N-glycosylation site:**

Amino acids 77-81;140-144;156-160

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 126-130

**N-myristoylation sites:**

Amino acids 56-62;72-78;114-120;154-160;233-239

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**FIGURE 301**

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT  
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAGAGACA  
GCCCTGTCTGGACACAGAGTTACTGTGGATTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT  
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAAAGCTAAAGCAAATTGAACAGG  
AAAAAAAAAAGAAGATGGGTTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC  
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT  
GATTACCAAACAGGATTCCCATTTTCGTCAAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT  
ACTTTAGGCTGTGTCAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT  
AATCGCAAACCTCAAGACTATCCCAAATATTCCGATGCACATTCAGCAACTCTACCTTCAGTTC  
AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC  
CTCAGCCACAACAAAATTAAATCTCAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAAT  
CTACTACAACCTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTCTTCTTAAATCT  
CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAACTGCAGACAAATGCTATGGATGGG  
CTAGTAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC  
AAAATCTTTGCCAAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA  
ATGCCTCCTGGTTTTGCCTTCTTCACCTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT  
ATACCCGAAAAATACTTCGACAACTTCCAAACTTCATACTCTAAGAATGTCACACAACAAA  
CTACAAGACATCCCATATAATATTTTAAATCTTCCCAACATTGTAGAACTCAGTGTTGGACAC  
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAAATAAT  
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT  
TTAACATACATTTCGTGTGGACCAAAATAAACTAAAAGAACCAATAAGCTCATACATCTTCTTC  
TGCTTCCCTCATATACACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA  
CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCACGAT  
GATCCTGACAATGCTCATGAGAGCCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT  
TATTATGAAAATCAAGAATTAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA  
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA  
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG  
AACTTACTCAAATAATGTAAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA  
ATTAAACGTTAATGGTTTCTTATGCTCTTTTTAAATATAGAAATATCATGTTAAAGAAAAAA  
AAAAAA

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**FIGURE 302**

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDYDQEPDDDYQTGFPPRQNVGYGVFPFHQYTLGCV  
SECFCPTNFPSSMYCDNRKLKTI PNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK  
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPFLPKSLERLLLGYNEISKLQTNAMDGLVNLT  
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSSISSIPEKY  
FDKLPKLHTLRMSHNKLQDI PYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEIEKM  
NLTVMCPSIDPLHYHHLTYIRVDQNKLEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ  
VFRFPDDDDDESEDHDDPDNAHESPEQEAGAEGHFDLHYENQE

**Important features:****N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

**Tyrosine kinase phosphorylation sites:**

Amino acids 268-275;300-307

**N-myristoylation site:**

Amino acids 230-236

**Leucine zipper patterns:**

Amino acids 146-168;217-239



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**FIGURE 303**

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC  
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA  
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCTGGT  
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT  
ACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT  
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT  
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGGACCTCCA  
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA  
AGGAGTAGCTGAAACCTTGACAGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA  
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG  
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG  
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCCTCAATGCTGCCAACGACGCTGA  
CCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT  
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCCAAAATCAGGAGGATGCCCCGAGACA  
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG  
CACTGTGGTATTAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA  
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAACTTTGTATTTAGTTT  
TTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACATAAATAATTTGAGTTTAG  
GTGATCCACCCCTTAATTGTACCCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT  
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAGCAAATAAAAG  
CTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAACA

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**FIGURE 304**

MNLVDLWLTRSLMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDLP  
PETVLLYLDSNQITSIPNEIFKDLHQLRVNLNSKNGIEFIDEHAFKGVAETLQTLDSLSDNRIQ  
SVHKNAFNNLKARARIANNPWHCCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLNAA  
NDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKKADEP  
DDISTVV

**Important features:****Signal sequence:**

Amino acids 1-33

**Transmembrane domain:**

Amino acids 204-219

**N-glycosylation sites:**

Amino acids 47-51;94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation sites:**

Amino acids 37-43;45-51;110-116

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**FIGURE 305**

CGCCACCCTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTCCACTTTGTTGAATTGTTCCCT  
ATACTCAAAATTGCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGAAATACGCAATGGAATTGAAGCCTGCT  
ATTGCAACATGGGATTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGT  
CCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCA  
GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG  
ATAATGTCTGTATAGCTGCAAAATATTAATAAACTTTAACAAAAATCAGATCCATAAAGAACCTGTGGCTTTGC  
TACAAGAAGTCTATAGAAATTTCTGTGACAGATCTTTCACCAACAGATATAATTACATATATAGAAATATTAGCTG  
AATCATCTTCATTACTAGGTTACAAGAACAACACTATCTCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTG  
AATTTGTAAAAACCGTGAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA  
GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCCAAAAGA  
CCACAGAGTTTGATACAAATTCACCGGATATAGCTCTCAAAGTTTTCTTTTTGATTCATATAACATGAAACATA  
TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG  
GCAATGTTGCAGTTGCATTTTATATTATAAGAGTATTGGTCCTTTGCTTTCATCATCTGACAACCTTCTTATTGA  
AACCTCAAAATTATGATAATTCTGAAGAGGAGGAAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAA  
ACCCACCCACATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA  
GTCTATGTGCATTTTGAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT  
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCAATTTTGATGTCTCTGGTCCTT  
CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTCTGATTTGTCTTG  
CCATATGCATTTTACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTACAAAAATCTTTGCT  
GTAGCCTATTTCTTGCTGAACCTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA  
TTGCCGGACTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGCATACATCTCTATCTCA  
TTGTTGTGGGTGTCATCTACAACAAGGGATTTTGCACAAGAATTTTATATCTTTGGCTATCTAAGCCCAGCCG  
TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCAGAA  
ACAACCTTTATTTGGAGTTTATAGGACCAGCATGCCTAATCATTCTTGTAAATCTCTGGCTTTTGGAGTCATCA  
TATACAAAGTTTTTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAA  
GAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCCTGGATCTTTGGGGTTCTCCATGTTGTGCACGCATCAG  
TGTTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTTCATTTTTTTTATTCTGTGTTTTAT  
CTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAGGTAAACAT  
AGAGAATGGTGGATAATTACAACGACAAAAATAAAAATTTCCAAGCTGTGGATGACCAATGTATAAAAAATGACT  
CATCAAATTATCCAATTATTAACACTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAACT  
GTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGTTTTCTATGTGAAATAGTTCTGTCAAAAAATA  
GTATTGCAGATATTTGGAAAGTAATTGGTTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTA  
ACACGAGAAGTATATGAATGTCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACT  
AGTCCCCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGAATATCAA  
CAGTGAAAAGGGAATGATAAGATGTATTTGAATGAACCTGTTTTCTGTAGACTAGCTGAGAAATTGTTGACAT  
AAAAATAAGAATTGAAGAAACACATTTTACCATTTTGTGAATTGTTCTGAACTTAAATGTCCACTAAAACAACCTT  
AGACTTCTGTTTGCTAAATCTGTTTCTTTTTCTAATATTCTAAAAAAGGTTTACCTCCACAATTGA  
AA

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**FIGURE 306**

MKRLPLLVFSTLLNCSYTONCTKTCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC  
TNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIANINKTLTKIRSIKEPVALLQEVYRNS  
VTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTLSNSTLTFVKTVNNFVQRDTFVVWDKLSVNHRRTHTLTKL  
MHTVEQATLRISQSFQKTTEFDTNSTDIALKVFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAF  
YYKSIGPLLSSSDNFLKPKQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNY  
SPDTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW  
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGLLHYFFLAFAWMCIIEGHLHYLIVVGVIN  
KGFLHKNFYIFGYLSPAVVVGFSALGYRYYGTTKVCWLSTENNFWSFIGPACLIILVNLLAFGVIIYKVRHT  
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEY  
YRLFKNVPCCFGCLR

**Important features:****Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 431-450; 494-515; 573-594; 619-636; 646-664

**N-glycosylation sites:**Amino acids 15-19; 21-25; 64-68; 74-78; 127-131; 177-181;  
188-192; 249-253; 381-385; 395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 360-364

**Tyrosine kinase phosphorylation sites:**

Amino acids 36-44; 670-677

**N-myristoylation sites:**Amino acids 38-44; 50-56; 52-58; 80-86; 382-388; 388-394;  
434-440; 480-486; 521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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**FIGURE 307**

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT  
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGC  
CCGGAGGAGCGCCTTCCCTGCCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA  
GGCCGGGCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA  
AGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTCAGAAAAGCGCAACAGAGAAT  
GCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA  
ATTCCTGTCTTGGCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT  
GCCTCACAAGGCATCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATG  
TCAACAAGCTGAGTGCCCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCTGA  
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC  
TGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAA  
TGGAGGGACCTGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA  
ATGCCCACAACCTGTGCAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGG  
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAACAAATGCCA  
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGC  
AGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTA  
CATCTGGTGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGTT  
GAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC  
TGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCTTGTTTCAGTGCT  
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTTCAGTGTGTAGTTGGCAGATATTTTCAAAT  
TACAATGCATTTATGGTGTCTGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAA  
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATTGTCAGATATTTAGATGTTTGTAC  
ATTTTAAAAAATGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATTCA  
GTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTTAAACAATATAATATATTCTAAACACAATGAAATAG  
GGAATATAATGTATGAACCTTTTGCATTGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCT  
AATAAACATTTTATACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTGGAAAAAAAAAAAAAAAAAA  
AAAAAAA

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**FIGURE 308**

MARRSAFFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM  
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLLGT  
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGCRNG  
GFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN  
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVCEPGCG  
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDPPESNYIW

**Important features:****Signal sequence:**

Amino acids 1-28

**N-glycosylation sites:**

Amino acids 88-92;245-249

**Tyrosine kinase phosphorylation site:**

Amino acids 370-378

**N-myristoylation sites:**

Amino acids 184-190;185-191;189-195;315-321

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 285-293

**EGF-like domain cysteine pattern signatures:**

Amino acids 198-210;230-242;262-274;294-306;326-338

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**FIGURE 309**

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGGG  
TTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT  
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGAACCCGAGCAATGGAG  
ATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG  
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTTCGATG  
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCGGAGGGG  
TTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAGGGCGCTA  
CAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGATAATTCCA  
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATAACAAGACAT  
ATAGACATGGAGAGAAGCTAATCATCACTTGTCATGAAGGATTCAAGATCCGGTACCCCGACC  
TACACAATATGGTTTTATTATGTGCGGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG  
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT  
TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAACTTGATGGGTCTGCGT  
ATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTGCCTTGCTCTGGAAG  
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCTGCCACCCGCGGCCTT  
GTGAGCGCTACAACCACGGAACGTGTTGGTGGAGTTTTACTGCGATCCTGGCTACAGCCTACCA  
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTCTTATCAAGTCTACTGCA  
TCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGACCACGTGGAAGATTGTGG  
CGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA  
CCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAGTTCCAGCAGTGACCCTGACT  
TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATGACGAAGCTGTGAGTGGCGGCT  
TGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCTTACCCGTGGACG  
ACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGACACAGGCCAGGGGAGTCAGAAA  
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTCACCTCCAGGTGCC  
AAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATAATTGCCAGCACGGCAGAGGAGGTGG  
CATCCACCAGCCCAGGCATCCATCATGCCCACTGGGTGTTGTTCTTAAGAACTGATTGATTA  
AAAAATTTCCCAAAGTGTCTTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTTGATTC  
CTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAAATTGCTATGCTG  
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCCTGTTTCTTCTTGACACAGACTGATTAA  
AATTAAAAGNAAAAA

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**FIGURE 310**

MYHGMNPSNGDGFLEQQQQQQQPQSPQRL LAVILWFQLALCFGPAQLTG GFDDLQVCADPGIP  
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ  
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG  
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLPPMVS  
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH  
ETLLTTWKIVAFTATSVLLVLLLVLARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML  
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDSVSGSSEL  
LQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

**Important features:****Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



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**FIGURE 311**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG  
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG  
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAGGCT  
CGTGCCCACCACCAAGTTCAGTGCCGCACCAGTGGCTTATGCGTGCCCCCTCACCTGGCGCT  
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA  
CCCAGAAAGGGCAATGCCCAACGCCCCCTGGCCTCCCCTGCCCCTGCACCGGCGTCAGTGA  
GCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGC  
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT  
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA  
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG  
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG  
ACAGTCTGGAAGCCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC  
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCCACTGG  
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGACCTCGCTGCCCTTGAG  
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA  
TGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC  
TCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA  
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC  
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA  
TTAAAGTTGCTTC

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**FIGURE 312**

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSQAAGPSSGSCPPTKFQCRT  
SGLCVPLTWRCRDLDCSDGSDEEEECRIEPC TQKGQC PPPGLPCPCTGVSDCSGGTDKKLRN  
CSRLACLAGE LRCTLSDDCIPLTWRC DGHDPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES  
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLLLLSW  
LRAQERLRPLGLLVAMKESLLLSEQKTS LP

**Important features:****Signal sequence:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 231-248

**N-glycosylation sites:**

Amino acids 126-130;195-199;213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation sites:**

Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;

224-230;230-236;263-269

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

**Leucine zipper pattern:**

Amino acids 17-39

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**FIGURE 313**

CGGACGCGTGGGCGTCCGGCGGTTCGAGAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGGCCCCAGCCCACAC  
CTTCACCAGGGCCCAGGAGCCACCAATGTGCGCATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC  
TTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGAC  
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG  
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC  
CTCGGCGTGCCACCCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG  
TACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC  
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCAT  
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCCCTCGGTCATGAACATGCATGAAATTTATACAGTGCTGAACCC  
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCCAACCTGATTCATGAGCCTCTTGACCAAGG  
CAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA  
CATGACGCCTGTCTGTGCCCCAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG  
TCTCGATGGTGCCTGTTGGTTCTGCGTCGCGGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGA  
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCAC  
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCCTGTCTACCGCCTCGGCTCCAA  
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT  
CCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC  
CCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC  
CAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGA  
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTGCGGGCACACGC  
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGGCCCCAATGGGGCGGTGACCCCAGCCTCGCCCCA  
CAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGGCGCGGGTTCGCTGACGCAGCGCCCCGCTGGG  
AGCCGCGGGCAGGCGAGACTGGCGGAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG  
CACAGCTGCAGATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC  
CAATACCCACCCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCAGGTGGAG  
TGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCAAGTGACCCTCCACCTCAGCCTCTCAAG  
TAGCTGGGACTACAGGTGCACCACACCTGGCTAATTTTGTATTTTGTAAAGAGGGGGGTCTCACTGTGT  
TGCCAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGG  
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAATAAAA  
CCAAAGTATTGATAAAAAAAA

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**FIGURE 314**

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCA  
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNRCT  
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**Important features:****N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

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**FIGURE 315**

CGGACGCGTGGGCCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT  
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCCAGCTGCCCAGGAC  
CCAGGGAACTGGAAGCCAGCAAAGTTGTCTCCTGCCCAGTTGTCCCGGAGCTCCAGGAAGTC  
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA  
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT  
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG  
GGGGCGGCTGGCTGGTGTTCAGAGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT  
CCTCCTACAGAGCAGGTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC  
ACCAGCTTACTCTCCAGGGTAACTGGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC  
GTACTTTGCCCCACTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC  
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCTGAGCCTCCACAGTGGGAGGCCCTTTA  
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT  
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG  
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC  
GGATGATGCTTCGATAGGGCACTCTGGCAGCCAGTGCCCTTATCTCTCCTGTACAGCTTCCGG  
ATCGTCAGCCACCTTGCCTTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAAT  
CATTTTAGCCCTTTCA

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**FIGURE 316**

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVVLLPSCPGAPGSPGEKGAPGPQG  
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCDMDTEGGGWLVFQRRQ  
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDFNGNRTFAHYATFRL  
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL  
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

**Important features:****Signal peptide:**

Amino acids 1-16

**N-glycosylation site:**

Amino acids 178-182

**Glycosaminoglycan attachment site:**

Amino acids 272-276

**Tyrosine kinase phosphorylation site:**

Amino acids 188-197

**N-myristoylation sites:**

Amino acids 16-22;89-95;144-150;267-273

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 242-255

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**FIGURE 317**

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGGTGTGCGGGGCCCAACCCCAGGAT  
GCTCCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT  
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCCACAGCTACACGGAATGCACAGATGGCTA  
TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCTGAGGC  
CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGCTACTTGTGCCTGCCCGCTCCGC  
TGCCGTCATCAACGACCTACATGGCGAGGGACCCCGCCACCAGTGCCTCCCGCTCAACACCC  
CAACCCCTGCCACACAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG  
TGCCCAGGCCCTGCACGACTGTGCCCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCA  
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGCCG  
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCGAGCC  
GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC  
CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCTGTGTCGCTGCCACACAGGGCTA  
TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT  
CTGTACGTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCACACAGGTTACCA  
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAGTGCTC  
CGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT  
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCGGCCTCCAACCTCTATGTGCG  
AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCGC  
TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTCAGATCCG  
TGCTGGAAACTCGCAGGGGGGACTTTTACATTAGGCAAATCAACAACGTCAGCGCCATGCTGGT  
CCTCGCCCCGGCGGTGACGGGGCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA  
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCCTACAC  
CTTCTGAGGAGCAGGAGGGAGCCACCTCCCTGCAGCTACCTAGCTGAGGAGCCTGTTGTGA  
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCCTGGTGGCTGAGGTGGGCGGGTC  
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCAGGCCAAGTTCACCTA  
AATGGGGGTCTCTATATGTTACAGGCCAGGGGCCCCATTGACAGGAGCTGGGAGCTCTGCAC  
CACGAGCTTCAGTCACCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCGGC  
CCAGAGATTTGGACTTGGCTGGCTTGCGAGGGGTCTAAGAACTCCACTCTGGACAGCGCCAG  
GAGGCCCTGGGTTCATTCTTAACCTCTGCCTCAAACCTGTACATTTGGATAAGCCCTAGTAGTT  
CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAA

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**FIGURE 318**

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPD SQHCRDVNECLTIPE  
ACKGEMKCI NHYGGYLCLPRSA AVINDLHGEGPPPPVPPAQHPNPCPPGYEPDDQDSCVDVDE  
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCE  
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDEC SYSSY  
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCSAQTCVNFHGGYRCVDTNRC  
VEPYIQVSENRLCPASNPLCREQPSSIVHRYMTITSERSVPADV FQIQATSVYPGAYNAFQI  
RAGNSQGDFYIRQINNVSAMLVLARPV TGP REYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF

**Important features:****Signal sequence:**

Amino acids 1-25

**N-glycosylation sites:**

Amino acids 198-202;394-398

**N-myristoylation sites:**Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;  
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270



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**FIGURE 319**

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC  
TCAAAGGTGCGTACCCAGCTGTGCCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGATGC  
CCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG  
GGGGAGCCCTGCGACCAACTCCACGTCTGCGAGCCAGCCAGGGCCTGGTCTGCCAGCCCCGGG  
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG  
AACGGCCGCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC  
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCCAGCTGGGAC  
TGCCCCCACCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA  
GGAGGGGGACTGGGGACCCAGCCCCCTCCAGCCCAAGGACCCAGTTTTCTGGCCTTGTCTCT  
TCCCTGCCCCCTGGTGTCCTTGCCAGAATGGAGCACGGCCTGGGGACCCTGCTCGACCACC  
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG  
CGCCGCCTGTGCCTGTCCAGGCCCTGCCACCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC  
TTCTTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC  
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCAGGCCCTTGGCTGCAGGCAACACTTTAGC  
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCGAGGTA  
TGGCAGAGGTGCAAGACCTAGTCCCCTTTCCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT  
GTCCAGGGTCCTCTAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG  
CGAGCTTTCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC  
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG  
AGATTCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAATAATTGTTCTGAATACAAGCCTAT  
GCGTGA

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**FIGURE 320**

MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVPLVLDGCGCCRVCARRLGEP  
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEGDG  
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGGLGTQPLPAQGPQFSGLVSSLP  
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRRLCLSRPCPPSRGRSPQNSAF

**Important features:**

Signal sequence:

Amino acids 1-23

**N-myristoylation sites:**

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;  
167-173;183-189;209-215

**Insulin-like growth factor binding proteins signature:**

Amino acids 49-65

**von Willebrand C1 domain:**

Amino acids 107-124

**Thrombospondin 1 Homology Block:**

Amino acids 201-216

**IGF binding protein site:**

Amino acids 49-58

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FIGURE 321

[illegible]

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## **FIGURE 322**

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAVI  
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 3-9, 26-32

**Amidation site.**

amino acids 68-72

**Small cytokines (intecrine/chemokine).**

amino acids 23-88

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**FIGURE 323**

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCA  
TGCCCGAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCTGGGCTCAGTGCTGTGAGGCTCGGCCA  
CGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG  
TCCCCGAGGGCATCCCCACCGAGACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAACGCTCAACCAGGACG  
AGTTCGCCAGCTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCGCCT  
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCA  
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTACATGTTTCAGG  
ACCTGTACAACCTCAAGTCACTGGAGGTGGCGACAATGACCTCGTCTACATCTCTACCGCGCCTTCAGCGGCC  
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGC  
ACGGCCTCATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC  
GACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAACTGCCTCTACGGCCTCAACC  
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC  
GCTTCTCAACCTCTCCTACAACCCCATCAGCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG  
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCCTCAACTACCTGCGCGTGC  
TCAATGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA  
TCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGGCGCCGCTGGCGGCTCAACTTCA  
ACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC  
TGCCCAACTACTTCACCTGCCGCCGCGCCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCC  
ACACGGTGAGTTTGTGTGCCGGGCCGATGGCGACCCGCGCCCGCCATCCTCTGGCTCTACCCCGAAAGCACC  
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCTACGCCCAGGTAC  
AGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGACTCCATGCCCCGCCACCTGCATGTGC  
GCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAG  
AGGCCAACAGCACCCGCGCCACTGTGCCTTTCCTTCGACATCAAGACCTCATCATCGCCACCACCATGGGCT  
TCATCTCTTTCCTGGGCGTCTGCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACACAA  
AGCACAAATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCGACGCGCCCCGCAAGT  
TCAACATGAAGATGATATGAGGCGGGGCGGGGGCAGGGACCCCCGGCGCGGGGAGGGGAAGGGGCTGGT  
CGCCACCTGCTCACTCTCCAGTCCTTCCCACCTCCTCCCTACCCTTCTACACAGTCTCTTTCTCCCTCCCGCC  
TCCGTCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGG  
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT  
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTTTATGAAACTTGAAATAA  
TAAAAAGAGAAAAAACTAAAAA

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**FIGURE 324**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLSVLSGSATGCPPRCECSAQDRAVLCHRKCFVAVPEGIPTETRL  
LDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLSNLTKQDI  
SENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHL  
NINAIRDYSFKRLYLKVLKLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS  
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGNLETILDSNPLACDC  
RLLWVFRRRWRLNFNRRQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG  
DPPPAIWLSPRKHLVSAKSNGLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGND SMPAHLHVRSYSPDWPHQP  
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR  
KSDAGISSADAPRKFNMKMI

**Important features:****Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,  
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,  
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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**FIGURE 325**

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG  
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG  
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAGGAG  
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG  
AGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG  
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC  
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT  
TGGCATTGTTGGGGAAGTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCCTGGAGGGAC  
AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGGCAGGGGTCC  
CTCGGAGGCCTCCTGGGGATGGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGCGCTGGTACTC  
TGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC  
TACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA  
GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT  
CTTTATGACCCCTTTCTGCCCCCATTAAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAACC  
TTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT  
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCTGTTTGGAGCTCGCGAC  
GGAGCCGGCTCGGAACATCAGATCAACCACAGGGCTTCTCTGCTGAGGTGCAGCTCATTCAC  
TTCAACCAGGAAGTCTACGGGAATTTAGCGCTGCCTCCCGCGGCCCAATGGCCTGGCCATT  
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCAGTCGCCTCCTTAACCGC  
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG  
CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC  
TCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC  
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC  
CGGCCCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGCAACAGGGACCCCGGCACCCCGAG  
AGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGATGGTGTCCCCCATGGTCGCTGAGAC  
TCCCCTTCGAGGATTGCACCCGCCCCTCCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT  
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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**FIGURE 326**

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA  
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLY  
SHRLSELRLFLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN  
VASTSNPFLSRLNDRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW  
ILIDRALNITSLQMHSRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP  
NYRLHVDGVPHGR

**Important features:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 177-199

**N-glycosylation sites:**

Amino acids 118-122;170-174;260-264

**Eukaryotic-type carbonic anhydrases proteins:**

Amino acids 222-271;128-165;45-93



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**FIGURE 327**

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT  
TTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA  
GTAGTACATGGTGGATAACTTCTACTTTTAGGAGGACTACTCTCTTGACAGTCCTAGACTGGTCTTCTACACT  
AAGACACCATGAAGGAGTATGTGCTCCTATTATCCTGGCTTTGTGCTCTGCCAAACCCCTTCTTTAGCCCTTCA  
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG  
ATGATGATGAGGACAACTCTCTTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTCCATTTGATCTGTTTCCAA  
TGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA  
ACATTCCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG  
GACTCACTTCACTTTATGGTCTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAAAGCCTTTCTAACCA  
CAAAGAAGTTGCGAAGGCTGTATCTGTCCACAATCACTAAGTGAAATACCACTTAATCTTCCCAAATCATTAG  
CAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACG  
TTTTGGAAATGAGTGCAAACCCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTTC  
ATATCAGAATTGCAGAAGCAAACTGACCTCAGTTCTTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAG  
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAA  
ACAACAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCAGTGTGAGAGAAATACATTTGGAAAACA  
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCCCTTCAATTCTAATTCAA  
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT  
TATTCACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACATTTCTGTGTGTTTGGAGAGAATGAGTGTTTC  
AGCTTGGGAACCTTTGGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT  
TTGGAATACTTGAACCTTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGAAGTCC  
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAACTATTGATACATAAGGGGTGAGAGAAACA  
AGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGATCTTACATAAATCTCATGCTTGACCATTCCCTTCTTCAT  
AACAAAAAAGTAAGATATTCGGTATTTAACACTTTGTTATCAAGCACATTTAAAAAGAACTGTACTGTAAATGG  
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA  
AGAGTGCATTACACTATTCTTATTCTTTAGTAACTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA  
TTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGTCTTTATGTTTAAACTAATTTCTTAAAA  
TAAAGCCTTCAGTAAATGTTTATTACCACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT  
GCTTTTTTTTTTTAATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC  
CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTGTTAGGCTATATAACATTGCCACTTCAA  
CTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGACACTAACAATCTACACC  
AAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT  
CAAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAA  
CATATGTAAATCAGAAAACAGGGAAATTTTCATTAATAATATTGGTTTGAAT

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**FIGURE 328**

MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPTREPRS  
HFFPFDLFPMPFCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS  
LYGLILNNNKLTKIHPKAFLTTHKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT  
FKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI  
STVELEDFKRYKELQRLGLGNKKITDIENGLANI PRVREIHLENNKLKKIPSGLPPELKYLQI  
IFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

**Important features:****Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

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**FIGURE 329**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA  
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT  
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGTGTT  
CAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGCTGGCGTACTGCCTGCACCAGCG  
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT  
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC  
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGA  
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA  
TGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT  
GTTTGCTTGGGAGAGAGACTGAGGAAGAAGTATGTGGAAGACATTCCCTTTCTTTCACCAAC  
CTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCG  
TTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCATCCACACTGATGA  
AGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG  
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAGGTGAAGGA  
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC  
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA  
GAGAGCTGTGGACACATCCTTGTACATACTGCCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC  
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC  
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT  
AATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAGT  
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT  
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA  
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA  
TGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAAATAAAGTGCCTTTATACAATG

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**FIGURE 330**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVFRHGARSPLKPLPLEEQVE  
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKKNYVEDIPFL  
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQ  
PGISEDLLKKVKDRMGIDSSDKVDFILLDNVAAEQAHNLPSCPMLKRFFARMIEQRAVDTSLYILPKEDRESLQMA  
VGPFLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ  
LYYHGKEQVPRGCPDGLCPDMLNAMS SVYTLSP EKYHALCSQTQVMEVGNEE

**Important features:**

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

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**FIGURE 331**

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACATTTTCCCTTTTCCT  
AACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTTGCTGGAGAAGAAAGGGCTGAGGGCAG  
AGCAGGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCCCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT  
GCAGCGGAGTGAGGTGATGGAAGTCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA  
CCTGGAGAGCCTGGGGGAGGGCCTGCCTAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG  
ACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGGTGAACCTCAACAGCCT  
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAAATAAAATTTTAA  
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGG  
GAGAAAGTATGTTAAAAATAGAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACC  
CTGGGTCAGGCCAGCCTCTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTTGTTTGCAGAA  
TCATGTGAGGGCCAACCGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCTCTC  
AGCATGGAACAGAGGCAGCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCTGCTCTCAGTGGTC  
TGGGTGCTGCTGGCCCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACC  
TTCAACCACTTGACCGTCCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACA  
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC  
GTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC  
CGCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG  
GAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGC  
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCAGCCTGTCC  
AGCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCT  
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT  
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC  
TTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGC  
TGCACCCGGGCGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAG  
GCCTTCAATATACACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAGGGCAGAAGCAGTATCACCACCCG  
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGAGATCAAGGAGCGCCTGCAGTCCTGC  
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCC  
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTG  
TACACCACAGCAGGGACCGCATGACCTCTGTGGCTCCTACGTTTACAACGGCTACAGCGTGTTTTTGTGGGG  
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTTCAAGATGCTCCAATGCCATTACCTCCTCAGCAA  
GAGTCCCTCTTGAAGGTAGCTATTGGTGGAGATTAACTATAGGCAACTTTATTTCTTGGGGAACAAAGGTGA  
AATGGGGAGGTAAGAAGGGTTAATTTTGTGACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTAT  
GTAAGGAATGCAAGCGTATTTCAATATTTCCAACTTTAAGAAAAAAGTTAAGAAGGTACATCTGCAAAAGCAAA

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**FIGURE 332**

MGTLGQASLFAPPGNYFWS DHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR  
ALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNHLTVHQGTGAVYVGAINRVYK  
LTGNLTIQVAHKTGPEEDNKSRYPP LIVQPCSEVLTLTNNVNKLLIIDYSENRL LACGS LYQG  
VCKLLRLDDL FILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLF IGTAVDGKQDYFPTL  
SSRKLPRDP ESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDI FYIYGFASGGFVYFLTVQPE  
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSL AQ  
AFNITSQDDVLF AIFSKGQKQYHHPPDDSALCAFP IRAINLQIKERLQSCYQGE GNLELNWLL  
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVV FVGT  
KSGK LKKVRVYEFRC SNAIHL LSKESLLEGSYWWRFN YRQLYFLGEQR

**Important features:****Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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**FIGURE 333**

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAGG  
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTACGC  
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGGCCCTGAT  
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCA  
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTACGTACGGCCAGACCAGCCTGGACAGGCT  
TAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG  
GGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTC  
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT  
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT  
GGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA  
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC  
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG  
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGGTGTGTGCAA  
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAGGTGGCGTCTGAT  
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA  
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA  
TGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATAACCGGTCTGATAGAGGA  
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCG  
GGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAA  
GTTCCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA  
GAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGC  
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAAGTTGTGGCCACCTT  
CCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC  
CACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT  
GGACATAG

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**FIGURE 334**

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGQ  
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALNDTQ  
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF  
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK  
NGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY  
PVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS  
RLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

**Important features:****N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157



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FIGURE 335

CCCAGAAAGTTCAAGGGCCCCCGGCCTCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCAG  
AGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTGCT  
GCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCAAAGA  
CCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAAAGAA  
GACTGTTTCTCCAGATTAGAGTGGAAGAACTGGGTGCGAGTGTCTCCTTTGTCTACTATCA  
ACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCGGATCAA  
AAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTGAGCAAGG  
CCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCCATCATG  
TGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGACAAAGAAGG  
GAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAAATCCCAGACT  
TGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACCTGGAAGTCTGCAATTTAA  
TACTGTTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTCTGTTGGATATCG  
CAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGT  
AGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGG  
CTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAG  
TGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGGCGGGATC  
ACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATAC  
AAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGGAGACAGGAGAATC  
ACTTGAACCCGGGAGGCGGAGGTGTCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGG  
TAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATACTGGTTTTTACC  
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

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**FIGURE 336**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW  
KKLGRSVSFVYYQQTLLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV  
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSS  
YTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVALVIS  
VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

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**FIGURE 337**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCGG  
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA  
TGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG  
CCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG  
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTCATCCC  
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT  
TGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT  
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTACAGCTGCT  
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCTTAGAACTCA  
ATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA  
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC  
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC  
TCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCA  
CTGCCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG  
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCC  
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC  
TGCCCTGGCCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCG  
CACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTC  
TCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCTCAACCAA  
TATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATTGATGACCCCACTCATTGGCTAAAG  
GATTTGGGGTCTCTCCTTCCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAG  
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA  
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC  
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT  
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT  
CTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG  
GTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAACTAACATGAAATATGTGTT  
GTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAAA

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**FIGURE 338**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS  
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPYSC  
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQWDR  
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAADVAG  
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTLSSVTS  
ARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSSGLSRMGAVPV  
MVPAQSQAGSLV

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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**FIGURE 339**

CGGAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTTGGCGCTTTTCGATCCACCCTCCT  
CCCTTCTCATGGGACTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA  
GGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCGTCTTCATCGTCGCGGTTTC  
TGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCCGGACGAGACGAAGTTCGCCAGCAGACAGTGGCCCCACAGC  
AACAGAGGGCGAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC  
CGTGACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTTGCCTGCTATGTACAGTTTGTAAAT  
CAGGTCAAACAAATAAAAGTTCTGTACCACGACAGACACCGTGTGTAGTGTGAAAAAGGAAGCTTCCAGG  
ATAAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTGAGTAATTGTA  
CGCCCCGGAGTGACATCAAGTGCAAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAAACCCAGCAGCGGAGGAGA  
CAGTGACCACCATCCTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTTT  
TAGCTGTGGTTGTGGTTGGCTTTTCATGTCCGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG  
GAGGAGTCCCGAACGTGTGCACAGAGTCTTTTCCGGCGCGTTCATGTCTTCCAGAGTTCCTGGGGCGGAGG  
ACAATGCCCGCAACGAGACCCCTGAGTAACAGATACTTGACAGCCACCCAGGTCTCTGAGCAGGAAATCCAAGGTC  
AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAG  
CTGAAGGGTGTGAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGCACCTTGCTGG  
ATGCCTCGGCAACACTGGAAGAAGGACATGCAAAGGAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT  
TTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCTGTGAAGAATCTCTTCAGGAAACAGAGCTTCCCT  
CATTTACCTTTTCTCTACAAAGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAACACT  
CTACTATCCAATATGGGGCAGCTTACCAATGGTCCTAGAACTTTGTTAACGCACTTGAGTAATTTTTATGAAAT  
ACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGTATTAAGG  
GTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTT  
GAGCTCGGGAGTTTGTAGACCAGCCTCATCAACACAGTGAAGTCCATCTCAATTTAAAAAGAAAAAAGTGGTTT  
TAGGATGTCAATCTTTGCAGTTCTTCATCATGAGACAAGTCTTTTTTCTGCTTCTTATATTGCAAGCTCCATCT  
CTACTGGTGTGTGCATTTAATGACATCTAAGTACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTTA  
ACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTTCAGTTCGGATATTTTTGACTTAATGATGAGATTATC  
AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTTGAGCTTTAAGATA  
GGATTATTGGGGCTTACCCACCTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGCTGTACATCTCTT  
TTCCGATTTTTGTATAATGATGTAAACATGGAAGAACTTTAGGAAATGCATTATTAGGCTGTTTACATGGGTTG  
CCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG  
AGGCACTTACTGCATTCAGTTCTCCCTCCTGCCCTGAGACTGGACCAGGGTTGATGGCTGGCAGCTTCTCA  
AGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTTATTT  
ATTTATAAGTAGATGTTTACATATGCCCAGGATTTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGTCTGGTTT  
GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG  
ATCCGAGACTGCGAAGAGCTTCTCTTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTTGGG  
CTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGGACGGTGTCTGGG  
AATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCCCTCTCGCTTCTGGTGGTCTGTGAACAGTCCCT  
GGGATGCCTTTTAGGGCAGAGATTCTGAGCTGCGTTTTAGGGTACAGATTCCCTGTTTGGAGAGCTTGGCCCCCT  
CTGTAAGCATCTGACTCATCTCAGAGATATCAATTTCTAAACACTGTGACAACGGGATCTAAAATGGCTGACACA  
TTTGTCTTGTGTACGTTCCATTATTTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACCTCT  
TCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTC  
AAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTGGCTGGGACAAAGTTAGAAGTGCCTGAAGTTCGCACATTTCAG  
ATTGTTGTGTCCATGGAGTTTATAGAGGGGATGGCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATC  
TGGCGTCCCACACCTTGTCCCCTGCACTTCTGGATGACACAGGGTGTGCTGCTGCCCTCTAGTCTTTGCCTTTGCTG  
GGCCTTCTGTGCAGGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCCTTCCCTC  
AGAGGCCTTCTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTAAGCTTATTCTTTAACATAAGCTTC  
CTGACAACATGAAATTGTTGGGGTTTTTGGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCCGGGCCAAAT  
AGCATAAACACCTGGTTATATATGAATACTCATATGTTTATGACCAAAATAAATATGAACCTCATRTTAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 340**

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPPQQTVAPOQQQR  
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTCQCEKGSFQDKN  
SPEMCRTRCTGCPRGMVKVSNCTPRSDIKCKNESAASTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIILAV  
VVVGFSCRKKFISYLKGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQEL  
AELTGVTVESPEEPQRLLEQAEAGCQRRLLVPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE  
EDEAGSATSCL

**Important features:****Transmembrane domains:**

amino acids 35-52, 208-230

**N-glycosylation sites.**

amino acids 127-131, 182-186, 277-281

**Glycosaminoglycan attachment site.**

amino acids 245-249

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 260-264

**N-myristoylation sites.**

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

**TNFR/NGFR cysteine-rich region.**

amino acids 99-139

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**FIGURE 341**

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG  
CCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCAGG  
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC  
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTCCAGGATCGCGAGGCAGCAGCGA  
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGTACTTC  
GCTTTCTCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC  
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC  
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAACCTGGCTC  
TGTTCTGTTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAATGTTTG  
TGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG  
ATTGGAATGACAACCCCCGAAAAATTTCTGGGTATTCTCTGGAGATACTGGTCAAAGAAGATA  
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG  
CTTCCCTGCTGGTGGTGA CTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG  
CCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCAGCTATTCATTAAC T  
TCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCAAGGGGTTTATGGCAAATTACTGCC  
ATGGAGAGTGTCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG  
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC  
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTACGACATTATGAAGACATGG  
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTTCTTAGGG  
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

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**FIGURE 342**

MLRFLPDLAFSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQVPYILKKIFQDREAAAT  
TGVSRDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ  
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRVWPWPQGAVHFNLLDVAKD  
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRKRRAA  
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNYAFMQA  
LMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 112-116, 306-310

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 96-100

**N-myristoylation site.**

amino acids 77-83

**TGF-beta family proteins.**

amino acids 264-299, 327-341, 345-364



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**FIGURE 343**

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCCTTTTCATTGACAACTGACTTTTTTTATTTCT  
TTTTTTCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
CTGTGTTTTGGGGTTTCTTCTTCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGG  
GCTCAGTGCTTGCCTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCTGCTCTGTCTTTACTTCAAATACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCCCTTCCAGGAAGGAGTTGGGGAGAGAGAAACCCTCACTGTGGGAATGCTGATAAACCACTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGGCTGGCTGGAAGTACGCTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGTCTTAAAGGCTGCCCAGCGCCTTGCCAAAATGGAGCTTGTA  
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTCTCTCTAACATCTCTATTCCAACTGT  
GGCGGTTACCTGGATACCTTGGGAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT  
TGTGTGTGGCACAACAAGTGGAGAAAGATTACAAGATAAACTAACTTCAAAGAGATTTTCTAGAAAATAGAC  
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTCTGACTGTCTGTGTGTCTACAGATTATGCCAATTC  
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAACCTTGAGACCAAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAACAACCTCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAAGTCAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCAATTCA  
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTCTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAAATGCCTTTAAATTCCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGAT  
AGCAGTGACCACAGTCTCGCTGCAATCAAGGTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTCTGTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTACGCAT  
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTCATGGTTCTAGCTCTG  
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

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**FIGURE 344**

MELVRRRLMPLTLLILSCLAELTMAEAEAGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE  
RPENKSIRIIFSIVQLDPDGSCESENIKVFDTSSNGPLLQVCSKNDYVPVFESSSSTLTTFQ  
IVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD  
YKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTIVLSTDYA  
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV  
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNSTVEIIYI  
TEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPNLVVFLDT  
CRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD  
SSDHQSRCNQGCVSRSKRDISSYKWKTDIIGPIRLKRDRSASGNSGFQHETHAEETPNQPFN  
SVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Important features:****Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

**FIGURE 345**

TGGGGGCCCCCAAGGCTCGCGCGTGGAGCGAAGCAGCAATGGGCAGTCTCGGTGCGCGCTGGCCCTGGCGGTGCTCTC  
GGCCTTGCTGTGTCAAGTCTGGAGCTCTGGGGTGTTCGAAGCTGAAGCTGCAGGAGTTCGTCAACAAGAAGGGGCT  
GCTGGGGAACCGCAATTGCTGCCGCGGGGGCGCGGGGCCACGCCGTGCGCCTGCCGGACCTTCTTCCGCGTGTG  
CCTCAAGCACTACCAGGCCAGCGTGTCCCCGAGCCGCCCTGCACCTACGGCAGCGCGCTCACCCCGTGCTGGG  
CGTCGACTCCTTCAGTCTGCCCGACGGCGGGGGCGCGGACTCCGCGTTACAGAACCCCTACCGCTTCCCTTCCG  
CTTCACTGGCCGGGACCTTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTGATGACCTGCACACAGA  
AAACCCAGAAAGACTCATCAGCCGCTGGCCACCCAGAGGCACCTGACGGTGGGCGAGGAGTGGTCCCAGGACCT  
GCACAGCAGCGGCGCACGGACCTCAAGTACTCCTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGGGGCTG  
CTCCGTTTTCTGCCGTCCCCGGGACGATGCCTTCGGCCACTTCACCTGTGGGGAGCGTGGGGAGAAAGTGTGCAA  
CCCTGGCTGGAAGGGGCCCTACTGCACAGAGCCGATCTGCCTGCCTGGATGTGATGAGCAGCATGGATTTTTGTGA  
CAAACAGGGGAATCGAAGTGCAGAGTGGGCTGGCAGGGCCGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG  
TCTCCATGGCACTGCCAGCAGCCCTGGCAGTGCACCTCCAGGAAGGCTGGGGGGGCTTTTCTGCAACACAGGA  
CCTGAACTACTGCACACACCATAAAGCCCTGCAAGAATGGAGCCACCTGCACCAACACGGGCCAGGGGAGCTACAC  
TTGCTCTTGCCGGCCTGGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCAGCCCTTGTAA  
GAACGGAGGGAGCTGCACGGATCTCGAGAACAGCTACTCTGTACCTGCCACCCGGCTTCTACGGCAAAATCTG  
TGAATTGAGTGCATGACCTGTGCGGACGCGCCTTGCTTTAACGGGGGTGCGTGCTCAGACAGCCCGATGGAGG  
GTACAGTGGCGCTGCCCGTGGGCTACTCCGCTTCAACTGTGAGAAGAAATGACTACTGCAGCTTTCAACC  
CTGTTCTAATGGTGCCAAAGTGTGTGGAACCTCGGTGATGCCTACCTGTGCCGTGCCAGCCGGCTTCTCGGGGAG  
GCACTGTGACGACAACGTGGACGACTGCGCCTCCTCCCCGTGCGCCAACGGGGGCACCTGCCGGGATGGCGTGAA  
CGACTTCTCCTGCACCTGCCGCGCTGGCTACACGGGCAGGAAGTGCAGTGCACCCGCTCAGCAGGTGCGAGCACGC  
ACCTGCCACAATAGGGGCCACTGCCACAGAGAGGGGGCCACCGCTATGTTGTGCGAGTGTGCCCGAGGCTACGGGG  
TCCCAACTGCCAGTTTCCGTGCTCCCCGAGCTGCCCGGGGCCAGCGTGTGTGAGCTCACTGAGAGCTAGAGGG  
CCAGGGCGGGCCATTCCCTGGGTGGCGTGTGCGCGGGGTATCCTTGTCTCATGTGCTGCTGGGCTGTGC  
CGCTGTGGTGGTCTGCGCTCGGGTGTGAGGCTGCAGAAGCACCGGCCCCAGCCGACCCCTGCCGGGGGGAGACGGA  
GACCATGAACAACCTGGCCAAGTGCACGCGTGTAGAAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATCAA  
GAACACCAACAAGAAGGCGGACTTCCACGGGGACCACAGCGCCGACAAGAATGGCTTCAAGGCCCCGTACCCAGC  
GGTGGACTATAACCTCGTGCAGGACCTCAAGGGTGACGACACCCGCGTACGGGACCGCGCAGCAGCAAGCGTGACAC  
CAAGTGCCAGGCCACGGGCTCCTCAGGGGAGGAGAAGGGACCCCGACCACTCAGGGTGGAGAAGCATCTGA  
AAGAAAAAGGCCGAGTCTCGGCTGTTCACCTTCAAAGACACCAAGTACCAGTCGGTGTAGCTCATATCCGAGGA  
GAAGGATGAGTGCCTCATAGCAACTGAGGTGTAAATGGAAGTGAGATGGCAAGACTCCCGTTTCTCTTAAATA  
AGTAAATTTCAAGGATATATGCCCCAACGAATGCTGCTGAAGAGGAGGGAGGCCTCGTGGACTGCTGCTGAGAA  
ACCGAGTTCAGACCGAGCAGGTTCTCCTCCTGAGGTCTCGACGCGCTGCCGACAGCCTGTCGCGGGCCCGCCGCC  
TGCGGCACCTGCCTTCCGTGACGTGCGCGTGTGCACCTGAGCAGTGTGCTTAAAGAAATATATATTTAAATGGGT  
GAATGAATTACGACATAAGAAGCATGCAGCTGAGTGTATATTTGGATTCTTATGAGCAGTCTTTTTCTTGA  
ATTAGAAACACAACACTGCCTTTATTGTCTTTTTTGATACGAAGATGTGCTTTTTCTAGATGGAAGAGATGTGT  
GTTATTTTTTGGATTTGTAAAAATATTTTTTCATGATATCTGTAAAGCTTGAGTATTTTGTGATGTTTCGTTTTTA  
TAATTTAAATTTTGGTAAATATGTACAAAGGCACCTCGGGTCTATGTGACTATATTTTTTGTATATAAATGTAT  
TTATGGAATATTGTGCAATGTTATTTGAGTTTTTTACTGTTTTGTTAATGAAGAAATTCCTTTTTAAATATTT  
TTCAAAATAAATTTTATGAATGACAAAAA  
AAAAAAA

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**FIGURE 346**

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVC  
LKHYQASVSPEPPCTYGSVATPVLGVDVSFLPDGGGADSAFSPNPIRFPFGFTWPGTFSLIIEA  
LHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDEHYGEGCS  
VFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR  
YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPKNGATCTNTGQGSYTCS  
CRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCADGPCFNG  
GRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD  
DNVDDCASSPCANGGTCTRDGVNDFSCTCPPGYTGRNCSAPVSRCEHAPCHNGATCHERGHRYV  
CECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWVAVCAGVILVLMLLLGCAAVVV  
CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKN  
GFKARYPAVDYNLVQDLKGDDTAVRDAHRSKRDTCQPPQSSGEEKGTPTTLRGGEASERKRPD  
SGCSTSKDTKYQSVYVISEEKDECVIATEV

**Important features:****Signal sequence:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 546-566

**N-glycosylation site:**

Amino acids 477-481

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 660-664

**Tyrosine kinase phosphorylation sites:**

Amino acids 176-185;252-261

**N-myristoylation sites:**

Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;  
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;  
676-682;683-689;695-701

**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 552-563

**EGF-like domain cysteine pattern signature:**

Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;  
467-479;505-517

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**FIGURE 347**

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAACA  
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTTCAGGCTCGCCAGCGCCCAGCCAG  
GGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCCTCGCTCCTGCTCCTGCTCCTGCTGT  
TCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGGACAT  
CTGATGAAACAGTGGTGGCTGGTGGCACCCTGGTGGTCAAGTGCCAAGTGAAAGATCACGAGG  
ACTCATCCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC  
TTCGAGATAATCGAATTTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA  
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG  
CCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTTATAAATCTT  
CATTACGGGAAAAAGACACAGCCACCCCTAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC  
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC  
CCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG  
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC  
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG  
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT  
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT  
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA  
AGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC  
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTGCTCATCATGCTCATCTTCC  
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG  
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA  
AGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCCTGCGCCCCCAGGGGCCCTGTGGGG  
ACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT  
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT  
TTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTTCGTGGCTT  
CTCTGCATTTGGGTTATTATTATTTTGTAAACAATCCCAAATCAAATCTGTCTCCAGGCTGGA  
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAAAAACA

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**FIGURE 348**

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQWS  
NPAQQTLYFGEKRALRDNRILVTSTPHELSSISISNVALADEGEYTCSIFTMPVRTAKSLVTV  
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT  
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL  
HCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN  
VNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTAEAGSDDAPDADT  
AIINAEGGQSGGDDKKEYFI

**Important features:****Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 349**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG  
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA  
GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTATTTTTTTTTTCTTTTTCTT  
TTTCCCACCACATTGTATTTTATTTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGG  
CTTTTTTCTGAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCCCTA  
GTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG  
AGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGCTGGATTTCTGCAGAACTGCACAATGTAC  
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTCAGAG  
TTCTCCATTTGCAGGAAAAACAATATTACAGACCATTTACGGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGC  
TGCACCTGGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCCTCAAAT  
TGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGG  
ATGAAAATCGAATTGCTGTCTATATCCGACATGGCCTTCCAGAATCTCACGAGCTTGGAGCGTCTTATTGTGGACG  
GGAACCTCCTGACCAACAAGGTATCGCCGAGGGCACCTTCAGCCATCTACCAAGCTCAAGGAATTTTCAATTG  
TACGTAATTCGCTGTCCCACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTGAGGACAACC  
AGATAAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC  
TGCGGATGCTGACTCAAGGGGTTTTTGTATAATCTCTCAACCTGAAGCAGCTCACTGCTCGGAATAACCTTGGT  
TTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCA  
TGTGCCAAGGTCCTGAACAAGTCCGGGGGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCA  
CGACCCCGGGCTGCCCTCTTTCACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTA  
TTCCAAACCTTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAAACTTCCCACGATTCTGACTGGGATG  
GCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCATTTGTGAATGATACTTCCATTC  
AAGTCAGCTGGCTCTCTCTTTCACCGTGATGGCATACAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAG  
GGGGCATCGTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA  
CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGCCA  
CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCACAGCATGG  
GCTCCCCCTTTCTGTGTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGCTCAGCGTCTTTT  
GCTGGCATATGCACAAAAGGGGCGCTACACCTCCAGAAAGTGGAAATACAACCGGGGCCGGCGGAAAGATGATT  
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCTGGAGATGACAGAAACCAAGTTTTTCAGATCGTCTCCTTAA  
ATAACGATCAACTCCTTAAAGGAGATTTACAGACTGCAGCCATTTACACCCCAAATGGGGGCATTAATTACACAG  
ACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTGACAGC  
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG  
ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA  
TGGGATTTAAÀAAAAGTGCTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACCTCTTGCTTTTTTAA  
TCTT

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**FIGURE 350**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE  
GVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISR  
AALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELRVDE  
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGT  
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD  
CSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMVRELNMNLLSCPTTTPGLPLFTPAPSTAS  
PTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVNDTSIQVSW  
LSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYRAV  
EDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVLLSVFCWHMH  
KKGRTSQQWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKGDFRLQPIYTP  
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Important features:****Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50



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**FIGURE 351**

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACGCGACCGC  
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCGCTGGGAGCTTCGGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC  
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC  
GAGCGCCCATGCCCCACTACCTGCCGCTGCCGCGGGGAGCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT  
CCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAACTGCATTTCCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA  
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAAACTGCCCACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAATTTTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT  
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATGGG  
AACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATTGCATTTAAATACA  
TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAACAACCTTTCAGAGCTTTGTA  
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTGCTGTTAGCCAGATGGCTTTGTGTGT  
GATGATTTTCCCAAACCCAGATCAGGTTTCAGCCAGAAACACAGTCGGCAATAAAGGTTCCAATTTGAGTTTC  
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTGGAAAAAGACAATGAACACTGTCATGAT  
GCTGAAATGGAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG  
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCATCTCCAATCACTTTGGTTCATCCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCAGCTTGGAGTGTGCTGTGTGGGGCACCCAGCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC  
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTTTTGCGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGCCGCTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAAGTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC  
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAAATACACATGTGAG  
ATGCTTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCACTCCCACTCCGACTCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTGT  
GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC  
AACACAGATGAGACCACTTGCCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGCTTTCAGAAAGTGGAAGCCACCACAGTTTGTCTCATCTTCAGGTGCTGGATTTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT  
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCAGATCCTTTTGAACA  
TATCATACAGGTTGCAGTCTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG  
GAGTGCTACCCATGTTCTCATCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC  
TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCAGTAATTCTTTCATGGGTACCTTTGGAAAA  
GCTCTCAGGAGACCTCACCAGTATGCTTCAAGCTTTGGACAGCCATCAGATTGTGAGCAAGAGCCTTTTAT  
TTGAAAGCTCATTTCTCCCAAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA  
GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAATTTTATTTAAAGAGAGAGAAT  
CTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAATGCTTTATTTATACAGATGAACCAAAATAC  
AAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTATTTTTTAACCTTG  
TTTTATGCAAAAAAGTATCTTACGTAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA  
TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACATTTTTTAAATAGAAGTT  
ACTTCATTATATTTTGCACATTATATTTAATAAATGTGTCAATTTGAAAAA

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**FIGURE 352**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCIGDLLDCSRKRLARLPEPLPSW  
 VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLETL  
 DLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNISAIPPKMFKLPQLQHLELNRN  
 KIKNVDDLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN  
 RISPDWFEFCQKLSELDTFNHLSRLDDSSFLGSLNLT LHIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI  
 EDMNGAFSGLDKLRRLLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLQQLHLNTSSLLCDC  
 QLKWLPPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS  
 SDSPMTFAWKKNONELLHDAEMENYAHLEAQQGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN  
 MLPSFTKTPMDLIRAGAMARLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS  
 CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTERHFFAAGNQ  
 LLIIIVSDVSDAGKYTCEMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSIV  
 WVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSST  
 CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDFETYHTGCSPPDPTVLMHDHYEPSYIKKKECYPCSH  
 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSNSFMGTFGKALRRPHL  
 DAYSSFGQPSDCQPRAFYLKAHSSPDLDGSGEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

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**FIGURE 353**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTCTCCTTTCTGGCTTCGGACATTGG  
AGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTACTTTGTGATGAGATCGGGGATGA  
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTAC  
AGGGGACGTTTGCAAAGAGAAGATCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAA  
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCGACTTCCCAGTTTTACCATTTATTTCTGCATGGCAATTCCTT  
CACTCGACTTTTCCCTAATGAGTTGCTAACTTTTATAATGCGGTTAGTTTGCACATGGAAAACAATGGCTTGCA  
TGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAAGATCAAGTC  
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATAT  
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACC  
TGCCAACGTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA  
GGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTGGGACTGCACCTGTGATCT  
GCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCAC  
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAACCGAGTGGATTCTAG  
TCTCCCGGCGCCCCCTGCCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCA  
AGAGGATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG  
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACAGTTTACCCTGCCCTGGGGGCTG  
CAGCTGCGACCACATCCCAGGGTCGGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT  
GAAGCCCAAGTCTCTAACGTGCAGGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTT  
TGTGGATTACAAGAACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAA  
GAACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGAGAAATTCGCGGG  
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCCTCCCGGGCCTTTCAATGCCAT  
GCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTC  
GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTC  
CATCATCCAGATAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA  
ACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTTTAGAAAGGATTTTCA  
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACCTTCGCACAGTAAAAA  
CAGCACTGGGTTGGCGGAGACCGGGACGCACTCCAACCTCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT  
GGTCCCGGGACTGCTGCTGGTGTGTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTGTTATCCTGAGGAA  
CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGTGACTC  
TTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGATGACTGTGGCTCTCACTCGCTCTC  
AGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCCGG  
GGCTGGAGGGGCGTGTAACCAATCCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC  
GCACAACCGAAAGGGCCTGACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA  
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCAGCAGCACCTGCTGGAAGAACTGACA  
GTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATACATATATACATATATCCACATC  
TATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTTGGCTACGCAGGGAT  
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACTTTGACTTCTGAC

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**FIGURE 354**

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYHL  
FLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQTF  
LGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLIILNDNLISTLPANVFQYVPITHLDLRGNRL  
KTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ GKDL  
NETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKIPGNW  
QIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLMKMNCRNRNVSSLADLKP KLSNVQ  
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE  
KFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNLLRSLPVDVFAGVSLSKLSLHNN  
YFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK  
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT  
SAFTTVGMLVFILNRKRKRKRRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS  
LSD

**Important features:****Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

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**FIGURE 355**

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCAGAATAACTCAGGGCTGCACCGGGCCTG  
GCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAACTGTTGGCCGCTGGGCCCGGGGGGATTCTTGG  
CAGTTGGGGGGTCCGTCGGGAGCGAGGGCGGAGGGGAAGGGAGGGGGAACCGGTTGGGGAAGCCAGCTGTAGAG  
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC  
GGGGCCTCAGAGAATGAGGCCGGCGTTGCCCCGTGTCCTCTTGGCAGGCGCTCTGGCCCCGGGCCGGCGCGG  
CGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA  
GCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCGTGCGGGCGCGAGCTGCG  
CGCTGTGCTCGCGCTCTCGGGCAGGCCAGGGCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACT  
GGAGCGCAGGCGTTCCCACTGCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCTGGCTGTCTCCGACCCCGG  
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT  
CCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG  
CAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTT  
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCC  
GATCTCAGTTACTTGATCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTG  
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCCTG  
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCTT  
TGGGGGGACCGGGGTGCCACCAAGGCGCCCGCCGGCCACTGCAACCAGCCCCGTGCCGAGAGAACATGGCCAAT  
CAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCTGAACAAGACAATTGAGTAACATCTATTCTGAGAT  
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC  
CCCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTTTCTGACTCCTCCTC  
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGGCTTGT  
CAAGCTCTGCTTTCACGAAAGCCCTCTTCCAGCCAAGGAAGGAGTCTATGGGCCCGCGGGCCTGGAGAGTGA  
TCCTGAGCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT  
GCGGGACAGAGCAGAGGGTGCCCTTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGACA  
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTACTTGTGTAAGTACAA  
TTTTCTGCAGAAATCCCCCTTCTCTAAATCCCTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC  
CCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGATGGTGATACTGGGGACCGGCTAGTGCTGGGGAGAGATATT  
TTCTTATGTTTATTCGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT  
AATTTACATTAATAATAATTTCTACCAAATGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTATATTGG  
TTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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**FIGURE 356**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALST  
VRAGAE LR AVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD  
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGAASN  
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR  
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATATSPVP  
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS  
KFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPSSQPRKESMGPP  
GLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Important features:****Signal sequence:**

amino acids 1-16.

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

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**FIGURE 357**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGAAGA  
AGACTAAAAATGGTGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTATCCTTTTAAACATAATCCTAATTTCC  
AAACTCCTTGGGGCTAGATGGTTTCTTAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTECTGGAGGTATTCCCACGAACACCACGAACCTCACCCCTC  
ACCATTAACCACATACCAGACATCTCCCCAGCGTCCTTTACAGACTGGACCATCTGGTAGAGATCGATTTCAGA  
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAACACAGCTACTAGAGATACCGCAGGGCCTCCCG  
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC  
AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTGTTATGTTTCATATTCAATAGAGAAA  
GATGCCTTCTTAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCTTACTGTT  
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTAATAAC  
CTCAACCAATTACAAATTTCTTGACCTAAGTGGAATTTGCCCTCGTTGTTATAATGCCCATTTCCCTTGTGCGCCG  
TGTAATAATAATTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAGTTTACGTCTA  
CACAGTAACTCTTTCAGCATGTGCCCCAAGATGGTTAAGAACATCAACAACTCCAGGAAGTGGATCTGTCC  
CAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTCTCCCCAGCCTCATCCAATTGGATCTG  
TCTTTCAATTTTGAAGTTTCAAGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
AAAATTTGCGGATCAGAGGATATGTCTTTAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAGA  
CTGAAAGTCATAGATCTTTCAGTGAATAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT  
GCCAGAACTCTGTAGAAAGTTATGAACCCAGGTCTTGAACAATTACATTATTTTCAAGATATGATAAGTATGCA  
AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
TTGGATCTAAGTAAAAATAGTATATTTTTGTCAAGTCTCTGATTTTCAAGCATCTTCTTCTCAAATGCCTG  
AATCTGTCAAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTCACCTTACAGAGCTGAGATATTTG  
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT  
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT  
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCCCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG  
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAATCCCTAAGTTTCTTGCCTTCTGGAGTTTTTATGGT  
ATGCCTCCAAATCTAAGAATCTCTTTGGCCAAAAATGGGCTCAAATCTTTAGTTGGAAGAACTCCAGTGT  
CTAAGAAGCCTGGAAGCTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTATCCAATGTTCC  
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC  
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTC  
AACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG  
GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
CAAAGTGTGATCTCCCTGGATCTGTACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
TCTGTATCTCTCTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT  
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATGTGTAT  
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAGAGAGAAA  
CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAACCTTTCCAGAGCATA  
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAGATAGCATTTTAC  
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAGAG  
TCCAAGTTCTCCAGCTCCGGAAGGGCTCTGTGGGAGTTCTGTCCCTGAGTGGCCAACAACCCGCAAGCTCAC  
CCATACTTCTGGCAGTGTCTAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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**FIGURE 358**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGGI  
PTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFSGL  
TYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYRNP  
YVSYSEKDAFLNLTKLVLSLKDNNTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLQ  
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPFRWFKNINK  
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNELQVYRASMNLSQAFSSLKSLKILRIR  
GYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE  
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDSLKNS  
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRDLHLHSTAFEELHK  
LEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTMESESLRTEFRGNH  
LDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPPNLKNLSLAKNGLKSFSWK  
KLQCLKNLETDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS  
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDVWFVWVNHTEVTIPYLATDVTVCVGPGA  
HKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFC KAKIKGYQ  
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQ  
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLEKPFQKSKFLQLRKRLC  
GSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

**Important features:****Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860



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**FIGURE 359**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC  
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGG  
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT  
GGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACA  
AGGAGCGCGGGCGCCGCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC  
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC  
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG  
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA  
ACTATGAGCCTCCGGGGAACGTGAAGGGGAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC  
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCCGGAAGATG  
CTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGAAGCATCAGACT  
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG  
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCCAACTTCCTTAG  
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAACAACTGAGGTCCCTT  
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA  
CCCATGTTCCCTATCCCAAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA  
GCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACCTACCCCATG  
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT  
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT  
CCAAGTCCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC  
TGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC  
TGAAGTCCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG  
TGTTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGGTGAAGAGGTGAGCTGTCCTCCTG  
TCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA  
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG  
GCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACCGGGCCCACACCTCTCCTGCCCCCTCCC  
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT  
GCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGATTCTAGGGG  
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGCAGGGACGAGGGAA  
GGAAAGTAACCTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

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**FIGURE 360**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL  
AAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC  
GHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCPSG  
YHCKNSLCEPIGSPEDAQDLPYLVTEAPSF RATEASDSRKMGT PSSLATGIPAFLVTEVSGSL  
ATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI  
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLASVFPAQD  
KPGELQATLDHTGHTSSKSLPNFPNTSATA<sup>Δ</sup>ATGGRALALQSSLPGAEGPDKPSVVSGLNSGP  
GHVWGPLLGLLLLPLVLGIF

**Important features:****Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

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**FIGURE 361**

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGG  
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT  
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG  
AGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGCTGCT  
CCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCCGG  
GCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGG  
CCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG  
ACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGGCGGGACCCGCGGGGGCCACCGG  
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCG  
GGTGCCTCCGCCGTCTGACGCACCCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA  
TTACGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA  
TGCCACCGTCTACCCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC  
TTTCTTCCAGTTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAG  
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC  
CAGCATCAAGACAGACAGCACCTTCTCCGATTTCTGGTGTACTCCGACTGGCACAGCTCCCC  
AGTCTTTGCTTAGTGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGA  
GGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGG  
TGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA  
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGG  
CAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCACGGTGGGGTGCTCTCTTCCTGGTC  
CTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGGCCGGCCCTTTTCTCAGAGAT  
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 362**

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG  
EKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD  
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFQFFGGWPKPA  
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

**Important features:****Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

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**FIGURE 363**

[illegible]

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**FIGURE 364**

MMWRPSVLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGRE  
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD  
TDRDGRVGEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATREELT  
AFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQFRDF  
RDLNKDGHLDGSEVGHWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT  
NYGEDLTRHHDEL

**Important features:****Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

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**FIGURE 365**

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCG**ATG**GGGACAAAG  
GCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA  
TTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG  
AAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA  
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC  
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT  
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG  
CCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGGCAGTGCTG  
ACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG  
ATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACA  
ACAGGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCA  
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT  
GTGGGGGTCATCGTGGCAGCCGTCTTGTAACCCGTGATTCTCCTGGGAATCTTGGTTTTTGGC  
ATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG  
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTG  
GTG**TGA**GCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT  
CTGGCCCCTGATGTCTGTAGTTTTCACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCC  
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC  
CCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTTGTTTAAAGTGTTTATTCCCCATTTCT  
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA  
TGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTTGAATAGG  
TATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA  
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCAT  
CTCTGGGGCCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC  
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTGTGGA  
GAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA  
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT  
CACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA  
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG  
CAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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**FIGURE 366**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWK  
FDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYT C MVSEEGGNSYGEVKVKL  
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNSSYV  
LNPTTGELVFDPLSASDTGEYSCEARNGYGT P MTSNAVRMEAVERNVGVIVA AVLVT LILLGI  
LVFGIWFAYS RGHFDR TKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262



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**FIGURE 367**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTCATTTTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTAAAT  
TTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCCTAACCACTGGATTTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACGTGTTTGAATTCAGAAAGGACCAACACCCAGATAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTGGTGTCT  
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
CCAGTTCAAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGT  
GCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCTTCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAATTGAGGTATTTGAACCTTGC  
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA  
TTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGATGATACAGTCCAGAT  
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACAACCCCTTGGAACTG  
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG  
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCCGGCCCTCCACATC  
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCAAGACATGGGGCGTACAAAGTCCGGATAGCTGT  
GCTCAGTGATGGTACGTTAAATTTACAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTTACTTTTC  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCACTCC  
AGTGGTCTGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTGACAGAGAAAACCTT  
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT  
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACC  
TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAACAACAGTTAACACAATAAAATCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAA  
GACAGTTTATTAATAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACA  
AAAAGAAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAAGCAGACAAAA

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**FIGURE 368**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS  
TNTRLLNLHENQIQIIVNSFKHLRHLEILQSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL  
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLMCNLREIPNLTPLIKLDELD  
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH  
NPWNCNCDILWLSWWIKDAPSNNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC  
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTVQDTGMYTCMVNSVGNNTASATLNVTAATTP  
FSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKFTTIPVTDINSGIPGIDEVMKT  
TKIIIGCFVAITLMAAVMLVIFYKMRKQHRQNHAPTRTVEIINVDDDEITGDTPMESHLMPAIEHEHLNHYS  
YKSPFNHTTTVTNTINSIHSSVHEPLLIRMNSKDNVQETQI

**Important features:****Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,  
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,  
422-428, 433-439, 531-537

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**FIGURE 369**

CAAAACTTGCGTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTCGAGTTTACAGATTTTACAGATACCAAATGGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG  
AGCCCGGGCCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCCTGTTCCAGGAGGGCGTGTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACAACCAGC  
TGGAAAAGATCTACCTGAGGAGCTCTCCCGGTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA  
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT  
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAGCTGGCAGACGCCGGGC  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC  
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT  
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAAGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCATCC  
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCTGGCCTTCCAGGGCC  
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCCAGTGGCCTGCCTCGCCGCGTGC  
GCACCTCATGATCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACAGGCCACAGGTGCACCGCGACGCCCTTCCGCAAGCTGCGCCTGCTGC  
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAACA  
AGATTAGTGCGGTGCCCGCAATGCCTTCGACTCCAGCCCCAACCTCAAGGGGATCTTCTCAGGTTTAAACAAGC  
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTTCTGC  
AGCACACGCCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCACGGCCAGACACATGC  
ACACACATCACACCTCAAACACCCAGCTCAGCCACACAACTACCCTCAAACCACCAAGTCTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCTGCCCTGGCACACACAGGCACCCA  
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
GTCCATCTGTCCGTCCGTTCCTGGAGAAGACACAAGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCT  
GGAATCACAAAAGCTGGCTTTTATTCCTTTCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
TGGCCCACCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT  
GTTCTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCTTTATTTTTTATTCTTTCTAAGGAAAAAATGATAAAAAAT  
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

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**FIGURE 370**

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRSG  
GHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCCGIDLREFPGDLPEH  
TNHLSLQNNQLEKIYPEELSRHRLETLNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNKLT  
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI  
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK  
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLSNQLREQG  
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYFLEELNLS  
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAAALARGALAGMA  
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP  
ANAFDSTPNLKGIFLRFNKLAVGSSVDSAFRRLKHLQVLDIEGNLEFGDISKDRGLGKEKEE  
EEEEEEEEEEETR

**Important features:****Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

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**FIGURE 371**

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG  
CCGGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTACCGCCCCCACCCTCCTTCTGCAC  
TGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTTTCCTTACCAGAGTCTGTGCATCGCCCCGGACCTGGCCGG  
GAGGAGGCTTGGCCGGCGGGAGATGCTCTAGGGGCGGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAG  
GAAGATGGGCTCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCCTTGCCCTGCGCTGGTCCT  
GAGTCGTGTGCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCGTGCGCTCCGGACCA  
TGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCAGGACCAGGGGCTCCCTGCTTCCCGGTGCTT  
GCGCTGCTGTGACCCCGGTACCTCCATGTACCGGGCAGCCGCTGCCCCAGATCAACATCACTATCTTGAAAGG  
GGAGAAGGGTGACCGCGGAGATCGAGGCCCTCAAGGGAAATATGGCAAACAGGCTCAGCAGGGGGCCAGGGGCCA  
CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGCCCTTTTC  
GGTGGGCCGGAAGAAGCCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCGACACGGAGTTCGTGAACCT  
CTACGACCCTTCAACATGTTTACC GGCAAGTTCTACTGCTACGTGCCCGCCCTCTACTTCTTCAGCCTCAACGT  
GCACACCTGGAACCAAGGAGACCTACCTGCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTGCGCA  
GGTGGGCGACCGCAGCATCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACG  
CCTCTACAAGGGCGAACGTGAGAAGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAGTGGCTACCT  
GGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCCACCTTCCACCCCTGCGCTGTGC  
TGACCCACCGCTCTTCCCCGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTCACTGAGACGCCCTGCACAC  
ACAGAAAGCCAAAGCGATCGGTGCTCCAGATCCCCGAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACAG  
GGCGGGGACCCGCGAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGG  
CGAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGGCGCACCGCGGCTCCAGTCCTTGGAATAATTAGGCAAATT  
CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGGTTGTTATTTTTGTCTTTCCAGCCAG  
CCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAGACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGG  
GTCAGGGGAGGGGCCGGGGCAGGAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTCTTGAGGG  
ATAGGTGGACCTTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGTGA  
TGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGCTCCAGGTTGGTAGAA  
GCAGCCGAAGGGCTCCTGACAGTGGCCAGGACCCCTGGGTCCCCAGGCCTGCAGATGTTTCTATGAGGGGCAG  
AGCTCCTTGGTACATCCATGTGTGGCTCTGCTCCACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATG  
CCTGCCACCTTGGCATCGGCTTTCTGTGCCGCTCCCACACAAATCAGCCCCAGAAGGGCCCCGGGGCCTTGGCTT  
CTGTTTTTTATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGGCTAAGCATCACCGCTTCCACG  
TGTGTTGTGTTGTTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCTCATCCAGGCCCTTGACCA  
GTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT  
GTTTCTCAGGCTCCTGTGAGCCTCAGTCTGAGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCA  
GGATTCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGG  
TTGCGGTGTCTCCACGGTGTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCCATAGCCCC  
TCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCCCCCAAACCCCGCTGCTCTC  
TTCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGCTTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGG  
TCCCTAAGTCCCTCTCTTTAAGAACTTCTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGAAG  
CAGAGCGCCACACTCGCTGCTTAAGCTCCCCAGCTCTTTCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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**FIGURE 372**

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRPS  
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG  
PKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFYCYV  
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVVRLYK  
GERENAI FSEELDTYITFSGYLVKHATEP

**Important features:****Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

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**FIGURE 373**

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCCG  
TTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGGAA  
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAATGC  
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTTCAGAGG  
ATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACCCAAAG  
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAACACTGTGACAAAGCAGAGTTCT  
TCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA  
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTGGTTCTTCC  
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAAAAAAGGATC  
CATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG  
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG  
AAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT  
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA  
ATACCAAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAAGTAG  
AAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA  
TGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAATGATGCATTGGTTTTCT  
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA  
TAGGACGTGTGTTGTCATTATTTGTAGTAGTAACCTACATATCCAATACAGCTGTATGTTTCTT  
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTTTTTAA  
TGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAAGAAGTGTTTTA  
AGAATAATAATTTTGCAAATAAACTATTAATAAATATTATATGTGATAAATTCTAAATTATGA  
ACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTTAAAAAATTTTAACAGGTCTTTA  
GCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAACCTTTTAG  
CTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT  
TTGCCTTCTCAAAATGTACAATAAGCAACTAAAGAAAATTAAAGTGAAAGTTGAAAAAT

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**FIGURE 374**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV  
KPKDVSLLWA AVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI  
IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMWIKISEDKQLAV  
CLKYAGVFAENAEDADGKDVFN TKSVGLS IKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG  
HIFNDALVFLPPNGSDND

**Important features:****Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,  
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,  
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250



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**FIGURE 375**

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT  
CTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAAGAAA  
AAAAATCATGAAAACCATCCAGCCAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG  
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA  
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA  
CCGGGTACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG  
GTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA  
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA  
GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTCTTCAGATAT  
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC  
GGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAA  
AATTACAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC  
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATAACATTTCAGAAGCCAA  
GGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC  
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT  
GGAAAACAGACCTTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA  
CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC  
AGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC  
TCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAG  
GCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA  
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA  
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGG  
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA  
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCCACAGA  
GTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAA  
CAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG  
GCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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**FIGURE 376**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNRV  
TRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPKTS  
RVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ  
GITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAVPSAE  
FQWKDDKRLIEGKKG VKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGHTNASIMLFGPGA  
VSEVSNGTSRRAGCVWLLPLLVLHLLKF

**Important features:****Signal peptide:**

amino acids 1-28

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**FIGURE 377**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGAA  
ATGTGGCTCAAGGTCTTCACAACCTTTCTTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG  
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCCAC  
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCACACA  
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACCAACAC  
AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTGATGAA  
GGCAATTACATCGTGAAGGTCAACATTGAGGAAATGGAAGTCTATCTGCCAGTCAGAAGATA  
CAAGTCACGGTTGATGATCCTGTGACAAAGCCAGTGGTGCAGATTATCCTCCCTCTGGGGCT  
GTGGAGTATGTGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC  
CAATGGCTAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTCTCCCCAAAAC  
AATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG  
AACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA  
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGTTGACCTTGGAGAG  
GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG  
ACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTTGCATCTGAGAAAGTA  
GCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA  
ACTCATTTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGACAGAAAGGAAAATCA  
TTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATTATATCCATGTGTCTTCTC  
TTCTATGGAAAAATATCAACCCTACAAAGTTATAAAACAGAACTAGAAGGCAGGCCAGAA  
ACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA  
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGGATTCCAAGCAGGTCTGTTCCA  
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC  
CCTGCCCAGCAGCAAGACCATCCAGAGTGAACTTTTCATGGGCTAAACAGTACATTCGAGTGAA  
ATTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAGTATATTAATCTGGAATCAGTGAAGA  
AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA  
TTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA  
ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTCTC  
CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCACATC  
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTT  
AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT  
ATTTCCAAATTTCTATCTTGTTATTTGTACAACAAAGTAATAAGGATGGTTGTCAAAAAACA  
AAACTATGCCTTCTTTTTTTTTCAATCACCAGTAGTATTTTTGAGAAGACTTGTGAACACTT  
AAGGAAATGACTATTAAAGTCTTATTTTTATTTTTTCAAGGAAAGATGGATTCAAATAAATT  
ATTCTGTTTTTGCTTTTAAAAA

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**FIGURE 378**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS  
VVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQKIQVTVDDPVTKPVVQIHPPSGAVEY  
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPII  
YYGPYGLQVNSDKGLKVGEVFTVDLGEAILEDCSADSHFPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD  
YVCCAYNNITGRQDETHFTVIIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKYQPYKVIKQKLEG  
RPETEYRKQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTVYEVIIQHIIQAQQQDHPE

**Important features:****Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 379**

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACAA  
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTGT  
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCAAGC  
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA  
TTAAGGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC  
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAACAGCTG  
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAACATTGAT  
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA  
GATGCCATTGTCCCCCGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT  
GCCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG  
GAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGG  
GCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCA  
ATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCCTGCAA  
ATAG

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**FIGURE 380**

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS  
GATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVARR  
QEGAPPQQSARRDRMPCRNFFWKTFSSCK

**Important features:****Transmembrane domain:**

amino acids 51-69

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 35-39, 92-96

**N-myristoylation sites.**

amino acids 64-70, 75-81, 90-96

**Amidation site.**

amino acids 33-37

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**FIGURE 381**

GGCGCCGGTGACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGCC  
GCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCGGGCCCGCGCCCCGCC  
CCGCGCCAGGTGAGCGCTCCGCCCCGCGCGAGGCCCGCCCCGGCCCCGCCCGCCCCGCC  
CGGCCGGCGGGGGAACGGGCGGATTCTCGCGCGTCAAACACCTGATCCCATAAACATTTC  
ATCCTCCCGGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCCGCCCTCGCCCTG  
TGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGCGGAGCG  
CGCCGAGCCTCGTCCCGCGGCCGGGCCGGGCCGTTAGCGCGGCGCCTGGATGCGGAC  
CCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCA  
ACCCCTACG**ATGA**AGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG  
CAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTG  
ACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTGCTGCCAGCCAG  
CGCATCTTCTGACAGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCGTGCCTGCCGC  
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGCGGCTGCCTTCACT  
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCT  
GCCACATTCACGGCCTGGGCCGCCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG  
CTGGGCCCCGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG  
CTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCTGCAC  
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC  
CTACTGCA<sup>2</sup>CCAGAACC GCGTGCCCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCGCCTC  
ATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGCCCTGGCCCCCTG  
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCA  
CTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA  
CGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC  
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCC  
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCG  
GCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTGACAGCCCGCCGGGCAACGGCTCTGGC  
CCACGGCACATCAATGACTCACCCCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCCGCTCACT  
GCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA  
GGCTGTTACGCAAGAACC GCACCCGAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGT  
GGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC  
CTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCT**TGA**CCCCCAGCGGACACAAGA  
GCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCACGCCGCCAAGCCAGCCGG  
GCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCTCCCTGATGGACGCCTGCCGCCGCCACC  
CCCATCTCCACCCCATCATGTTTACAGGGTTCGGCGGCAGCGTTTGTTCAGAACGCCGCCTC  
CCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGA  
CGTGGAATAAAGAGCTCTTTTCTTAAAAAA

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**FIGURE 382**

MKRASAGGSRLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIF  
LHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPATF  
HGLGR LHTLHLDR CGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNR  
ISSVPERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRAL  
QYLR LNDNPWVDCRARP LWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVATGP  
YHP IWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH  
INDSPFGTLP GSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT  
GDSESGALPSLTCSLTPLGLALVLWTVLGPC

**Important features:****Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425



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**FIGURE 383**

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTCCTGAACTTGTCTG  
AAGCCCTTGTCGGTAAGCCCTTGAACCTACGTCTTAAATCTATGAAGTCGAGGGACCTTTCGCTGCTTTTGTAGGG  
ACTTCTTTCCCTTGCTTCAGCAACATGAGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTCTGTCACCTTCTTTGA  
TTGGGGCTTTGATCCCTGAACCAGAAGTGAATTTGAAGTTCTCCAGAAGCCATTCTGCCATCGCAAGACCA  
AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA  
AACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA  
AAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGCTCTGGGCTATGGAAAAGAAGGAAAAGGTA  
AAATTCCCCCAGAAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGAAATGGACCAAGATCCCATGAAT  
CATTCCAAGAAATGGATCTTAATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT  
TTGAAAACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAGAAGATG  
AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTATAGAGATACATCTACCCTT  
TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAAAGAACATTTTATTTTTATACAATGTTCTTTCT  
TGCTTTGTTTTTTATTTTTATATATTTTTTCTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTT  
CTTTCTGATAAGTTATTGGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTC  
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACCACGACATGA  
GACCAGGTTATAGCACAAATTAGCACCCATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCAACATTT  
GAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCATGTTATAATGAAATAGTTTATGTGTAAGTGGCTCTG  
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT  
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGA  
GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTGAGACCAGCCTGACCAACACGGAGAAACCCCTATCTCTAC  
TAAAAATACAAAGTAGCCCGGCGTGGTGTGCGTGCCTGTAATCCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA  
TCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAA  
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG  
CTCCTAGTGATTGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATGTA  
TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCCTT  
CCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACATTGTATCATAAGATAAAGTAGTAAACCA  
GTCTACATTTTCCCATTTCTGTCTCATCAAAACTGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAG  
CACTTTGGGGGCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCT  
TGTCTCTACTAAAAATACAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAGGCTGA  
GACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGG  
TGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGACCTACAGCAGCTACTATTGAATAAATACCTA  
TCCTGGATTTT

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**FIGURE 384**

MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS LF  
HSTHKHNNQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPESTLI  
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVEDIFD  
KEDEKDKDGFISAREFTYKHDEL

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

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**FIGURE 385**

CTCCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCTC  
CCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTCC  
CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG  
ATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG  
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGAACCTC  
ACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA  
CTGATCTCTCTGTTCTGTTCCAGGACCCTGCTGTCTCCTCCCCTTCTCCACCTTCCAG  
CCTCTGGCTACAACACGCCTGCAGCCCCAAGGCAAAAGCTCAGCAAACCCAGCCCCCAGGATTG  
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCAAAGCAGGGGAAGACAGGGGCTGAGGCC  
CCTCCATTGCCAGGGACTTCCAGTACGGGACAGAAAGGACTTCTCAGTACACAGGAACCTCT  
CCTCACCCAGCGACCTCTCCTCCTGCGAGGAGCTCCCGCCCCCATGCAGCTGGACTCCACC  
TCAGCAGAGGACACCAAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCG  
ATGGTCCGCATAGTGGCCCCAGTCTGCTGGTGTGCTGAGCCTTCTGTGAGCCGAGGCCTGATC  
GCCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG  
AACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCCCCTTCCAGGCCCTT  
GAGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAG  
TTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC  
TGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCGGACTCC  
AGGGCTCTCCCCACCTCCCCAGGCTCTCCTCTTGATGTTCCAGCCTGACCTAGAAGCGTTT  
GTACGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGAGACTGGGACATCCCTGAT  
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCTCAG  
TGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGCCTCATGCCAGTGTGCGACCCCT  
GCCTTCTCTCCACTCCAGACCCACCTTGTCTTCCCTCCCTGGCGTCTCAGACTTAGTCCCA  
CGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCTGGGGTGAGACTGGGATTCTGGCTT  
CTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAAACGTGATTCTGGCCCCA  
CCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTCTAACAATGCCCAGT  
GACTGTGCACTTGGGCTGTGACGTCTCCACCTGCCCCAATAGATCTGCTCTGTCTGCGACACCA  
GATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTCCAGGCCTTGGTCAGGTGAGGTGCACAT  
TGCAGGATAAGCCCAGGACCGGCACAGAAGTGGTTGCCTTTNCCATTTGCCCTCCCTGGNCCA  
TGCCTTCTTGCCCTTTGGAAAAAATGATGAAGAAAACCTTGGCTCCTTCTTGTCTGGAAAGGG  
TTACTTGCCTATGGGTCTGGTGGCTAGAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGT  
CTAACACAGAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTG  
GAGAAGGGGTGCGGGGTGGTGGTAAAGTAGCACAATACTATTTTTTTTCTTTTCCATTATT  
ATTGTTTTTTAAGACAGAATCTCGTGCTGCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCA  
AACTCCGCCCTCCTGGGTTCAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG  
GCACGCACCACCACACCTGGCTAATTTTTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTG  
GCCAGGCTGGTCTTGAATCCTGACCTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCG  
GGATTACAGGCATGAGCCACTGTGTCTGGCCCTATTTCCCTTAAAAAGTGAAATTAAGAGTTG  
TTCAGTATGCAAACTTGGAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA  
TAGTCTCACCAGAGACTATCATTATTTGTTTTGTTGTACTTCCTTCCACTCTTTTCTTCTTC  
ACATAATTTGCCGGTGTCTTTTTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGC  
CTTTTCCACCTTATCGTTCCATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTT  
ATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

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**FIGURE 386**

MRLLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCSG  
TIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDQAGEYWCGVEKRGPD ELLISLFVFP  
GPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPGTSQ  
YGHERTSQYTGTSPHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRILAPV  
LVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGDVISM P  
PLHTSEEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

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**FIGURE 387**

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACATG  
GCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCGGAGG  
CGCCCGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGG  
**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCACACT  
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCA  
GAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAAGTGGTG  
ATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCC  
TTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGACAGATTGAACCTCTGAAGCCCAGTGAT  
GAGGGCCGGTACACCTGTAAGGTTAAGAATTACAGGGCGCTACGTGTGGAGCCATGTCATCTTA  
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT  
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATTACTGGCAGCGA  
ATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATTGACTACAACCAC  
CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTACCAGTGCACAGCA  
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGTATGTACAAAGCATC  
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCCTTGGTG  
TGGCTGCTAATCCGAAGGAAAGACAAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT  
CGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCT  
CGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG  
CGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG  
GGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAAGTCCACCATGCTAATCTGACCAAAGCAGAA  
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCT**TGA**ATTACAATGGAC  
TTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGT  
CACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCAGTGAGCATTGCACGGAACAGATT  
CAGATGAGCATTTTCTTATACAATAACCAAACAAGCAAAGGATGTAAGCTGATTCATCTGTA  
AAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTTGT  
TGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAAACTTTTAAT  
GTGGGATATTTTGTATCAGTGCTTTGATTCACAATTTTCAAGAGGAAATGGGATGCTGTTTGT  
AAATTTTCTATGCATTTCTGCAAATTTATTGGATTATTAGTTATTCAGACAGTCAAGCAGAAC  
CCACAGCCTTATTACACCTGTCTACACCATGTACTGAGCTAACCCTTCTAAGAACTCCAAA  
AAAGGAAACATGTGTCTTCTATTCTGACTTAACTTCATTTGTCATAAGGTTTGGATATTAATT  
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCCACTCTATACTA  
ATCTCACTATTTGTATTGAGCCCCAAAATAACTATGAAAGGAGACAAAATTTGTGACAAAGGA  
TTGTGAAGAGCTTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA  
ATGGAGCAATTGTGGATTTCCCTCAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTT  
CTGGAAGGAGAAAATACAACATGTCATTTATCAACGTCTTAGAAAGAATTCTTCTAGAGAAA  
AAGGGATCTAGGAATGCTGAAAGATTACCCAACATACCATTATAGTCTCTTCTTCTGAGAAA  
ATGTGAAACCAAGATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTA  
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG  
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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**FIGURE 388**

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
ITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL  
KVLVRPSKPKCELEGELETEGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH  
PGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLIFLLV  
WLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANSASRSQ  
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

**Important features:****Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

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**FIGURE 389**

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG  
CCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT  
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCCCCA  
AAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA  
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC  
AGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGAATGTGA  
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC  
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAAAGACTGA  
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA  
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTCCGAAATTCAGAGAGAAA  
AGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG  
AAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCCTGAGTAAATGTGTTCTGTATA  
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACAGCCCATATTTGAT  
GAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA  
GTATTTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAAATGAATGG  
AAATTCCTTAAAAAAAAA



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**FIGURE 390**

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC  
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC  
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRSSWV  
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEQIEGCI PKERS

**Important features:****Signal sequence.**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125



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**FIGURE 391**

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAACACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCGGGAAGGG  
AGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCGCCCCGCGCCTCTGCGCGCCCTGTCCGCCCCGGCCC  
AGCCCAGCCCAGCCCCGCGGGCCGGTCACACGCGCAGCCAGCCGGCCGCTCCCGCGCCCAAGCGCGCCGCTCTG  
CTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGGCGCCCCGGTGACCGTGACCCCT  
GCCCTGGGCGCGGGGCGGAGCAGGCATGTCGCCCGCCGGGACCGCTACCCAGCGCTGGCCCTGGTGCTCCTGGC  
AGTGACCCTGGCCGGGGTCGGAGCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGATCTGGAG  
CCGGGAGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCGCTGCCTGCGGGGCCCCGGGA  
GGAGTGGGAGCGGGCGCCCGCAGGAGCCAGGCCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCCAAGAGGGA  
GAAGTCGGCTCCGGAGCGCCTCCACCAGGTAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGAA  
GGCTGCCAACGATGATCACAGTGTCGTGGCCGTGAAGATGTGAGAGAGAGTTGCCACCTCTTGGTCTGGA  
AACCTTAAAAATCACAGACTTCCAGCTCCATGCCCTCCACGGTGAAGCGCTATGGCCTGGGGGCACATCGAGGGAG  
ACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTATGACGGAGCGTGGTGCGGGGAAGAAATGACCTCCA  
GCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCTCATCACTCAAGGGAGGAACCTCCTG  
GCTGAGTGACTGGGTGACATCCTATAAGGTGATGGTGAGCAATGACAGCCACACGTGGGTCACTGTGAAGATGG  
ATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCTACCCGTCCCCATGGT  
GGCCCGCTACATCCGCATAAACCTCAGTCTGTGTTGATAATGGGAGCATCTGCATGAGAATGGAGATCCTGGG  
CTGCCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAA  
GCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCAGAATTTA  
CAACATTGGAAAAAGCCACCAGGGCCTGAAGCTGATGCTGTGGAGATCTCAGATCACCTGGGGAGCATGAAGT  
CGGTGAGCCCGAGTTCCTACTACATCGCGGGGGGCCACGGCAATGAGGTGCTGGGCGGGAGCTGCTGCTGCTGCT  
GGTGCACTTCGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCTGGTGGAGGAGACGCGGATTCA  
CGTCTCCCCCTCCCTCAACCCCGATGGCTACGAGAGGCCTACGAAGGGGGCTCGGAGCTGGGAGGCTGGTCCCT  
GGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTTCCTGATTTAAACACGCTGCTCTGGGAGGCAGA  
GGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCCTGAGTGGTTTCTGTGCGAAAAATGC  
CACGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGGAAAAAATCCCTTTTGCTGGGCGGAACCTGCA  
GGGCGCGGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCCCTGGAAGACGAGGAACACACCCCCAC  
CCCCGATGACCACGTGTTCGCTGGCTGGCTACTCCTATGCCTCCACACACCGCCTCATGACAGACGCCCCGGAG  
GAGGGTGTGCCACACGAGGACTTCCAGAAGGAGGAGGGCACTGTCAATGGGGCCTCCTGGCACACCGTCTGCTGG  
AAGTCTGAACGATTTAGCTACCTTCATACAACTGCTTCGAAGTGTCCATCTACGTGGGCTGTGATAAATACCC  
ACATGAGAGCCAGCTGCCGAGGAGTGGGAGAATAACCGGAATCTCTGATCGTGTTCATGGAGCAGGTTTCATCG  
TGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAAAGGAATCCCAAACGCCATTATCTCCGTAGAAGGCATTAA  
CCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCCTCCTGAACCTGGAGAGTATGTGGTCACAGCAAA  
GGCCGAAGGTTTCACTGCATCCACCAAGAAGTGTATGGTTGGCTATGACATGGGGGCCACAAGGTGTGACTTCAC  
ACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGGAGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGC  
CAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACGCGTGGGTGACCCCTCCTGGGCCCTTGAGACTCGTCTGG  
ACCCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAGTGGACTCACTCACTGTTGTTTCTCTGTAATTCAG  
AAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCCCAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTT  
CTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCAGCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAG  
CCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGGGAGCCTGTCCGTTTCAAGAGCCTCTGGCTGCATAGAAAAGG  
ATTCTGGTGCTTCCCTGTTTGCCTGGCAGCAAGGGTCCACGTGCATTTGCAATTTGCACAGCTAAAATTGCAG  
CATTTCCCCAGCTGGGCTGTCCCAATGTTACCATTTGAGATGCTCCCAGGCGTCTAAGAGAATCCACCCTCTC  
TGGCCCTGGGACATTGCAAGCTGCTACAAATAAATCTGTGTTCTTTTGACAATAGCGTCATTGCCAAGTGCACA  
TCAGTGAGCCTCTTGAATCTGTTTAGTCTCCTTTTCAACAAAGGAGTGTGTTTCAAGAAAAGGAGAGAGAGGCTGA  
GATCATTACAGGAGTTTGTGGGCAGCAAGCATGGAGCTTCTTGACAAATTTCTGGGTCCATAAACAACCCCCAAA  
GTCCCTGCTGATCCAGTAGCCCTGGAGGTTCCCAAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCTGAAGGGCCA  
GAAAATTTAGCCTGGATCTCCTCTTTTACCTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTC  
TCTCTGCTTGAGGATTGCCCCCTGTGTGGAATTGAGTGCTCATGGGTTGGCCTCATATCAGCCTGGGAGTTATTT  
TTGATATGTAGAATGCCAGATCTTCCAGATTAGGCTAAATGTAATGAAACCTCTTAGGATTATCTGTGGAGCAT  
CAGTTTGGGAAGAATTATTGAATTATCTTGCAAGAAAAAGTATGTCTCACTTTTGTAAATGTTGCTGCCTCAT  
TGACCTGGGAAAAATGAAAAAATAAAGCAATGGTAAGACCCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 392**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPPPLPA  
GPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDSVR  
VAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCAGRN  
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNNGSGDMIFEGNS  
EKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTTTDDL  
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGA  
HGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGGSELGGWS  
LGRWTHDGDIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAAETRAVIAW  
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSASTHRLMTDARR  
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNR  
ESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLNPGEYVVTAKA  
EGFTASTKNCMVGYDMGATRCDFTLSTNMARIREIMEKFGKQPVSLPARRLKLGRKRRQRG

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**FIGURE 393**

GTCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCATCATTGCTGAAGTGGACCAAC  
TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAATACCAAGTGTGAGGGAAGTGCC  
ATAACATGCAGAACTCATAGTGGTGAAGGAGCTGCCAGGAACTGGGCCGGGAGGAGGCGGAGGCAAGCTGGGGCCGCTT  
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGAGCATCAATGACCACAGCCACGGTTTCCCAAAGGCGAGCAGGA  
GCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCCC  
TAACACCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCCTGGATGTCATTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTTCATTTTTGATCTGGTGTAACTGC  
CTATGACAAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAAATAG  
CCCTGCGTTTGTGCTGAGAGTTCACTGGCACTGGAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT  
GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCTCCAGAGGT  
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTCGACCTCTAGACTATGAAAAGAACCC  
TGCCCTACGAGGTGGATGTTGAGGCAAGGACCTGGGTCCCAATCCTATCCAGCCCATTGCAAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTACATGGGCTCCAGCCATCACTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTTATTGCTCTTGTCATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCATGC  
CACACTGGACAGAGAGCAGTGGCCCCAATATACCCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTCAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGA  
AGTCTCCACGCGGGGAAAACAACCTTACCCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCACTGAACATGAAGAGATGGCCGGCTTTGAGTTCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGCATCCAGTGTCTGTGTGGGTGAGCCTCTTGATGCCAATGATAATGCCCCAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC  
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGTCCCGGCCATT  
CCTTTTGACAACCATTTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCACCTCTTCATCTCAACCTCATAACGGGCGAGCTGTTGTCATGTCAATGTACCAATGCCAGCAGCCT  
CATTTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCATGTTTGTCAACAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGCGAT  
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTGGGTTGATCCTGGCTTTGTTTATGTCCATCTGCCG  
GACAGAAAAGAAAGGACAACAGGGCCTACAACCTGTGCGGAGGCGGATCCACCTACCGCCAGCAGCCCAAGGGCC  
CCAGAAACACATTTCAGAAAGGACAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT  
CGGGCAGTCCCACAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTT  
CCACCTCACCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGAGCACCAGGCGGAGAGCCGAGAGGT  
GCTGCAAGACACGGTCAACCTCCTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGAGAACCTGAACCTTCC  
CGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGACCTCTGAAGTTGCAGGCAGCCCCACAGGGAGGCTGGC  
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGCTCGGCCACCTCCTCTGCAACCTGAGACGGCAGCGACATCT  
CAATGGCAAAGTGTCCCCTGAGAAAGAAATCAGGGCCCCGTGAGATCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
TGCCTTCGCCGAGCGGAACCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTGAGCAAATCTCCAGCTGCT  
GTCCTTGCTGCATCAGGGCCAATTCCAGCCCAAACCAAACACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGGACCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCCGACCCGCGCTGGATGGCGAGACTCTCTTGGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG  
CAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCAGCATGCCCGTGGAGGCGCCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACCAAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG  
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGGTCCTGTGAACATACCTCAGACGCTT  
CTGGATCCAAGAACCAGGGCCTGAGGATCTGTGGAACAGGCTGGTTTCTAAATCTTGTAACTCACTAGCTAG  
CGGCGGCTGAGAACTTTAGGGTGAATGCTGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC  
TGACCAAAGCAGCCCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT  
TCCTGGCAAAACATATGTGGAGCACAAGGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT  
CAATAAAGGAAAAGCAGTAAAAA

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**FIGURE 394**

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVMKYQVSEEVPSGTVIGKLSQELGREERRRQAG  
AAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVDLATGDLALIHVEIQVL  
DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLTHTYTLSPSEHFALDVIVGPD  
ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESSLALE  
IQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPLDYEKN  
PAYEVDVQARDLGPNPIPAHCKVLIKVLDVNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA  
DDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS  
AKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVSYRIQDSPV  
AHLVAIDSNTGEVTAQRSLNVEEMAGFEFQVIAEDSGQPMLASSVSVWVSLLDANDNAPEVVQ  
PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTTIVARDADSGA  
NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGSPPQLQTRALLRV  
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE  
STYRQQPKRPQKHIOKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCLOAPFHLT  
PTLYRTLNRNQGNQGAPEAREVLQDTVNLLFNHPRQRNASRENLNLPEPQPATGQPRSRPLKV  
AGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAAFAE  
RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGSRSAIPDTPGSPARAGG  
QTDPEQEEGPLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD  
NVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSLEMLLEQRSSMPVEAASE  
ALRRLSVCGRTLSDLATSAASGMKVQGDPPGKGTGTEGKSRGSSSSSRCL

**Important features:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 395**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG  
CTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC  
AGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCAATGGGACGCCCCCGACCTCGTGCG  
GCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG  
GAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGGCCTTG  
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGTGGCAACTGGGTCCCTTACAGCT  
GGCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAATAAAGAT  
GGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCACACCCCTGCTACAACAGCAGCGAT  
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC  
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA  
GGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAAGTA  
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC  
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT  
GATGGTGCATCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT  
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC  
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTC

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**FIGURE 396**

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV  
GGNWVLTAAHCKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNHDLMLLQL  
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCEDAYP  
GQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLDWI  
KKIIGSKG

**Important Features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

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**FIGURE 397**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTAC  
TACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT  
ACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCACTG  
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGCTGCA  
GCATCTCTCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG  
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC  
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG  
TGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCGTGTCCATC  
CTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC  
AGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA  
TGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA  
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCCCTGGCAGCCGGG  
AGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC  
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACTTGG  
AGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGCCCTGGGGACTACCA  
AGTGGCTCTGGGAGCCCACTGCCCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCTCC  
TGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCCTCCT  
TCCTCTGGGGGAGGAGGGGTTCTTGAGGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAG  
CCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCAGGGACTATTTTCTGCACCA  
GCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTCACAGTGAGCTTCCAGGACC  
CAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAAAAAAAAAAAAA

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**FIGURE 398**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGRL  
FTESCSISPKLRSIAVYYDNPHMVPPDKCRCVGSILSEGEESPSPELIDLYQKFGFKVFSFP  
APSHVVTATFPYTTILSIWLATRVRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCLARQGD  
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSATLSPGASSRGW  
DDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEKGKE





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**FIGURE 400**

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHEG  
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWLPL  
AHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI  
TGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDFQPGC  
GLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFKKGICLSCRKNR  
CNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:****Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

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**FIGURE 401**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG  
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCTGT  
CAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC  
AACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCCTGGTACC  
AGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC  
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCTGTGTCC  
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT  
TTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCCTCTGCCTCCCATTTCTGCCCCTGA  
CCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGGTTAATAATA  
TTCAACATGTCAACAAC

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**FIGURE 402**

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSQYQQRAGS  
APRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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**FIGURE 403**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGCGCTGCAGCAGCTCCAGAAAGCAGCGAGTTG  
GCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCTCACAACAAGATGCTCAAGGTGTCAGC  
CGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCAGTCTCTCGCAGCTGCCGCGCGGTGGCTGCAGCCGGGGG  
GCGGTGCGACGGCGGTAATTTCTGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG  
ACAGTGAACAAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGATCA  
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATTC  
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG  
GAGGGGTCCCATTATCCACCTGCAAGCAGTGCCAGTGGTCTATCCAGCCCTGTTTGTGGTTCAGATGGTCA  
TACCTACTCTTTTTCAGTGCAAACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG  
ACATTGCCCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT  
CAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAAAGTCAAAACAAGAAGACAAA  
AACATTGCTGAGGCTGAGAGAAGCAGATTCGATACCAGCATCTTGCCAATTTGCAAGGACTCACTTGGCTGGAT  
GTTTAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAA  
TGAACAGTGTACCAAGGCATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTG  
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCAAGGGGTAAA  
GAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT  
TGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTCATGGGATCCAGAATAAATGGTGTGCAGATTGTGC  
TATAGATTTTGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA  
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGAAGA  
CCATGATGTATACATTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTACAAAAATGATAG  
CCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCACATATATTTGTATAATTATTTGAA  
AAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAATAAGAATCATTTGCTTTGAGTTTTATATTCCTTACACA  
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTACGAGA  
ACAACTTTGTAAATCTTCATAAGCAAAATGACAGCTAGTGCTGGGATCGTACATGTTAATTTTTTGAAAGAT  
AATTCTAAGTGAAATTTAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT  
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA  
AAAAAAAAAAAAA

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**FIGURE 404**

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD  
EVEDDYFRTWSPGKPFQALDPAKDPCLMKKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV  
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPGPSDK  
PTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTLLRPERSRFDTSILPICKDS  
LGWMFNRLDTNYDLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNEWCYCFQRQQDP  
PCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDRYGNEVMGSRINGVA  
DCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEDEGDDDDGGDDHDVYI

**Important features:****Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

**FIGURE 405**

[illegible]

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**FIGURE 406**

MTPQSLLQTTFLLSLLFLVQGAHGRGHREDFRFSQQRNQTHRSSLHYKPTPDLRISIENSEE  
ALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQHQE  
ESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDLQLLSQF  
LKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH  
SRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGEKVLGI  
VVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRETQTSCF  
CNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSAALCLVTIAAYLCSRVP LPCRKRPRDY  
TIKVHMNLLLA VFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLEGYNLYRLV  
VEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS  
LVSYITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVL TLLGLSLVLGLPWALIFFSF  
ASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLPISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504



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**FIGURE 407**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG  
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC  
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA  
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC  
TGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAAAGCTC  
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC  
TCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGCTCAGCTG  
CCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA  
CTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTAC  
AAGCGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT  
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAACGTGTGCCGGAT  
GTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC  
CCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT  
CACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCACAGCAGGCTGGGAA  
ATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG  
TGAAA

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## **FIGURE 408**

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY  
EADGSTNNGIFQINSRRWCSNLT PNPVNPVCRMVCSDLLNP NLKDTVICAMKITQEPQGLGYWE  
AWRHHCQGKDLTEWVDGCDF

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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**FIGURE 409**

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC  
GCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCGGCTTACACCTTCCCTCGATAGCGACTTCACCTTTACCTT  
CCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCTGAAGGCCCTCGCTGGAGATCGAGTACCAAGTTTTA  
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA  
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTACAGCACCATT  
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAAATATGGGAGAACAGGCACAAGAACAAGATTGGAAAG  
AAATATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC  
AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC  
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGAGCCATTCAAGTTTTAT  
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACTAGAGTACGTAACATTGAAA  
AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA  
AAAGTAGGAAACAGGTATAATTTTAAATGTGAAAATTAAGTCTTCACCTTCTGTGCAAGTAATCCTGTGATCCAG  
TTGTACTTAAAGTGTGTAACAGGAATATTTTGCAGAAATATAGGTTAACTGAATGAAGCCATATTAATACTGCAT  
TTTCCTAACTTTGAAAAATTTTGCAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC  
AGTCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGTAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT  
TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCCAA  
CTTTTCTCTATTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGSTTTTTG  
AGATTTTTATAACCAAATACATTTTCAAGTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATT  
CCAAAAGCTGACATTTTTCAGATTCTTAAAAACACAAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG  
AAATGAAGAATATAGTTTAAAAGCTTCCCTCCATAGGGACACATTTTCTTAACCTTAACTAAAGTGTAGGA  
TTTTTAAATTAATGTGAGGTAAAATAAGTTTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
TAATCATGTTATGTTAATTTTAAATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA  
TTGCTAAAATGATCTGGGCCTACCATAAAATAATATCTCCTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA  
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAAATTCACCTAAGTAGAACTATAAATAAATATCTAGA  
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
AAACTTTGGCTGTAGGTTTTTATTTTCTACAAGAAATCTGGTTTGAATTATTTTGTAAAGCAGGTACATTTTATA  
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAATAATTTTATTATAACAACCTTTTAT  
TAAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTTAA  
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC  
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTAAAGTTATGCCCATTATATAACGTTGTTTAT  
GACTACATTGTGAGTTAGAAACAACTTAAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
TCTTAGGCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT  
ATGATCAATTACCTTAATTTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
AGGTCAATAAGATCCTTGCCATATGAATACCCCTCCCTTTTGCCTGTTAAATTTGCAATGAGAAGCAATTTTACA  
GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTCTA  
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTGACTCCTTACCTAACAAATGAATTTGTTACATAATCTTCT  
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTACAGTAACTTCTTACCATATAAAAACGATAATTGCTT  
TATTTGGAAAAGAAATTTAGGAATACTAAGGACAATATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTAAATATTTCTAAAGACATACGTGTTATCTGCTT  
CATATGCTTTTTTTTAAATTTCACTATTCCATTTCTAAATTAAGGTTATGCTAAATTGAGTAAGCTGTTTATCACTT  
AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTT  
CATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCCTAGAGTTTGCTCTGATATGCATTTGGATGATTAAT  
GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTGTAATTTTATGGTAAAATTAATCCTTCTTA  
CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTAT  
GTGAAATTTTAAAGACATTGATTCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTG  
CTCAAACGCTTTTATCTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA  
AAATTATCAAGGAAAA

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**FIGURE 410**

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFYQPMPLKASLEIEYQ  
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFELIL  
DNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE  
SNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 411**

CCGAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCCAGAGTCA  
GTGACTCTGTGAAGCACCACATCTACCTCTTGCCACGTTCCACGGGCTTGGGGGAAAGATGGTGGGGACCAAG  
GCCTGGGTGTTCTCTCTCTGGTCTTGAAGTCAACATCTGTGTTGGGGAGACAGACGATGCTCACCAGTCACTA  
AGAAGAGTCCAGCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTGCCGACACCTGGAGAGCCCTGGTGAG  
TGGACAACATGGTTCAACATCGACTACCCAGGCGGGAAGGGCGACTATGAGCGGCTGGACGCCATTGCTTCTAC  
TATGGGGACCGTGTATGTGCCCCGTCCCCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGCGGGCAGCACT  
GGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCCCTGGCCAGAACTGC  
TCTAATTACACCGTAGCCTTCTCTGCCCCACAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGAGCCCATGG  
TCTCCCTGGAGCAAGTGCTCAGCTGCCTGTGGTCAAGTGGGGTCCAGACTCGCACACGCATTGTCTTGGCAGAG  
ATGGTGTGCTGTGCACTGAGGCCAGCGAAGAGGGTCAAGCACTGCATGGGCCAGGACTGTACAGCCCTGTGACCTG  
ACCTGCCCAATGGGCCAGGTGAATGCTGACTGTGATGCCTGCATGTGCCAGGACTTCATGCTTCATGGGGCTGTC  
TCCCTTCCCCGAGGTGCCCCAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAGCTGCTGACCCAG  
ACAGACAGTGATGGGAGATTCCGAATCCCTGGCTGTGCCCCTGATGGCAAAAGCATCCTGAAGATCACAAAGGTC  
AAGTTTGCCCCCATTTGTAATCACAATGCCCAAGACTAGCCTGAAGGCAGCCACCATCAAGGCAGAGTTTGTGAGG  
GCAGAGACTCCATACATGGTGTGAACCTTGAGACAAAAGCACGGAGAGCTGGGCAGAGCGTCTGTCTGTGCTGT  
AAGGCCACAGGGGAAGCCAGGCCAGACAAGTATTTTGGTATCATAATGACACATTGCTGGATCCTTCCCTCTAC  
AAGCATGAGAGCAAGCTGGTGTGAGGAACTGCAGCAGCACCAGGCTGGGGAGTACTTTTGCAAGGCCCAAGT  
GATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTCAACAGCATCTGATGAGACTCTGATGAGACTCTGT  
CCTGAGAGCTATCTTATCCGGCTGCCCATGATTTGCTTCCAGAAATGCCACCAACTCCTTCTACTATGACGTGGGA  
CGCTGCCCTGTAAAGACTTGTGACGGGAGCAGGATAATGGGATCAGGTGCCGTGATGCTGTGCAAGAACTGCTGT  
GGCATCTCCAAGACAGAGGAAAGGGAGATCCAGTGCAGTGGCTACACGCTACCCACCAAGGTGGGAGGAGTGC  
AGCTGCCAGCGGTGTACGGAAACTCGGAGCATGATTTGCTTCCAGAAATGCCACCAACTCCTTCTACTATGACGTGGGA  
CGCTTTGGCCATGTGTACATGGGGAACAGCCGTGAAGCATGACTGGCTACAAGGGCACTTTTACCCTCCATGTC  
CCCCAGGACACTGAGAGGCTGGTGTCTACATTTTGTGAGCAAGGCTGCAGAACTTGTCAACACCACCAAGTGTCTA  
CCTTTCAACAAGAAAGGGGAGTGCCGTGTTTCCATGAATCAAGATGCTTCGTGCGAAAGAGCCCATCACTTTGGAA  
GCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTTGGTGAAGACCCCATGGCTGAAGTGGAGATTCCATCC  
AGGAGTTTCTACAGGCAGAAATGGGGAGCCCTACATAGGAAAGTGAAGGCCAGTGTGACCTTCTGGATCCCGGG  
AATATTTCCACAGCCAGCTGCCAGACTGACCTGAACCTTCAATGACGAAGGAGACACTTTCCCCCTTCGG  
ACGTATGGCATTTCTCTGTGGAATTCAGAGATGAGGTCACTCAGAGCCACTTAATGCTGGCAAGTGAAGGTC  
CACCTTGACTCGACCCAGGTCAAGATGCCAGAGCATATCCACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG  
GGGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAATCAAAGGAGGAACAAAAGAGAAGACAGAACCTTCTCTG  
GTGGGCAACCTGGAGATTGCTGAGAGGAGGCTTTTAACTGGATGTTCTGAAAGCAGGCGGTGCTTTGTTAAG  
GTGAGGGCTTACCGAGTGAGAGGTTTCTTCCATGAATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG  
GAGCCTAGAATGGCTTCTTGTCCAACCTAGGGCTGGGGCCGCTTTGACAGTGTCTACAGGGCCCCAACGGG  
GCCTGTGTGCTGCTTCTGTGATGACAGTCCCTGATGCTTACTCTGCTATGTCTTGGCAAGCCTGGCTGGG  
GAGGAAGTGAAGCAGTGGAGTCTTCTCTTAAATTAACCCAAATGCAATTGGCGTCCCTCAGCCCTATCTCAAC  
AAGCTCAACTACCGTCCGACGGACCATGAGGATCCACGGGTTAAAAGACAGCTTCCAGATTAGCATGGCCAG  
CCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCCATCTATGCCTTTGAGAACCTCCGGGCATGTGAAGAGGCA  
GCACCCAGTGCAGCCCACTTCCGGTTCTACAGATTGAGGGGATCGATATGACTACAACACAGTCCCCCTCAAC  
GAAGATGACCTATGAGCTGGACTGAAGACTATCTGGCATGGTGGCCAAAGCCGATGGAATTCAGGGCCTGCTAT  
ATCAAGGTGAAGATTGTGGGGCCACTGGAAGTGAATGTGCGATCCCGCAACATGGGGGCACTCATCGGCGGACA  
GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGGACAGGGACCAAGCCATGTCTCAGCTGCCTGT  
CTGGAGTTCAAGTGCAGTGGGATGCTCTATGATCAGGACCGTGTGGACCGCACCTGGTGAAGGTCTATCCCCAG  
GGCAGCTGCCGTGCGAGCCAGTGTGAACCCATGCTGCATGAGTACCTGGTCAACCACTTGGCACTTGCAGTCAAC  
AACGACACCAAGTGAATACCATGCTGGCACCTTGGACCCACTGGGCCACAATATGGCATCTACACTGTCACT  
GACCAGGACCTCGCACGGCCAAGGAGATCGCGCTCGGCCGCTGCTTTGATGGCACATCCGATGGCTCCTCCAGA  
ATCATGAAGAGCAATGTGGGAGTAGCCCTCACCTTCACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCCTTC  
CAGTACCTCCAAAGCACCCAGCCAGTCCCTGCTGAGGCACTGTCCAAGGAAGAGTGCCCTCGAGGAGGAGCAG  
CAGCGAGCGAGCAGGGGTGGCCAGCGCCAGGGTGGAGTGGTGGCCTCTCTGAGATTTCTAGAGTTGCTCAACAG  
CCCCTGATCAACTAAGTTTTGTGGTACTTCACTCTTCTGCCCTCATTTTCACTGTGACAGCCATTGTGAGACTGA  
TGCACAACTGTCACTTGGTTAATTTAAGCACTTCTGTTTTCTGTAATTTGCTTGTGTTTTCTTCACTGCTTTA  
CTTACTTTGTCCCATGCTACTGATTGGCAGTGGCCCCACAATGGCACAATAAAGCCCCCTTTGTGAAACTGTTT  
TTTAAATGAAACACAAGAAATGGCCACTGGTAAACTCTGCAGCTTCACTGTACTTCACTTAAATGCCATTAAT  
GCAATATATACTTCTTCTTTTTCATGGTTTTGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAA  
ATAACCAATATAAAGCATATTTCTTGGCCTTGTCCACAGGACATAGGCAAGCCTTGATCATAGTTTCATACATAT  
AAATGGTGGTGAATTAAGAAATAAACAATACTTTTACTTGAATGTAAATAACTTATTTATTTCTTTGCTA  
AATTTGGAATTTCTAGTGACATTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTCTCTACCAAGTCTGG  
AAAGAACATCTCTGGTATCCACAATTACACAGGTTGCTAACTGTATTGTACATTTCCCTTTGCATTGCTT  
TGTTCTTGCTAGAAACCCAGTGTAGCCAGGGCAGATGTCAATAATGCATACTCTGTATTTGAAAAA

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**FIGURE 412**

MVGTKAWVFSFLVLEVTSVLGRQTM LTQSVRRVQPGKKNPSI FAKPADTLES PG EWTTWFNID  
YPGGKG DYERLDAIRFY YGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRP  
GQNC SNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS  
EEGQH CMGQDCTACDLTC PMGQVNADCDACMCQDFMLHGAVSLPGGAPASGA AIYLLTKTPKL  
LTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTS LKAATIKAEFVRAETPYMVMNP  
ETKARRAGQSVSLCCKATGKPRPD KYFWYHNDTLLDPSLYKHESKLVLRLKLQHQAGEYFCKA  
QSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFY YDVGRCPVKTCAGQQ  
DNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCTETR SIVRGRVSAADNGEP  
MRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVL PFNKKGS AVFHE  
IKMLRRKEPIT LEAMETNII PLGEVVGEDPMAELEI PSRSFYRQNGEPYIGKV KASVTFLDPR  
NISTATAAQTD LNFINDEGDTFPLR TYGMFSVD FRDEVTSEPLNAGKV KVHLDSTQVKMPEHI  
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLEFNLDVPESRRCFVKV  
RAYRSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACVPAFCDDQSPDA  
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPRVKKTAFQISMAKPR  
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTVPFNEDDPMSWTEDYLAWW  
PKPMEFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF  
KCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAVNNDTSEYTMLAPLDPLG  
HNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALTFNCVERQVGRQSAFQYLQ  
STPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFP RVAQQPLIN

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**FIGURE 413**

GCCACGTTGTCTTCTTTCCTTCACCACCACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC  
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGCCGTCTCTTGCCTCCTTCTC  
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCCCTTAGACTCCGTT  
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG  
AAGCTCTCGTGTGCTAGTGTCAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT  
GTCAGTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTTCTAGCTGGAAACCACCTGC  
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCGCTGCTGCCACCTGACCTGACAGGGA  
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT  
CTAACTCAAACGTCCCCTTCATTTGTTCCATTCTTGATTCTTGGGTAATAAAGACAACTTT  
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 414**

MGPSSCLLLILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS  
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT



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**FIGURE 415**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGTG  
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAGGA  
GTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTTGCC  
TGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGGG  
TGCCTCGAAGTGCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCAGCTTC  
ATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTT  
ATGAGGTTCTGTCAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAAGGATTAA  
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTTTGGTTTCA  
TGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAG  
ATCTAGAAGTCACCTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAAC  
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGATGCGGACCACCC  
AGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA  
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG  
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC  
GAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA  
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA  
AGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG  
GGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT  
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT  
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGTTT  
AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTTGTGTGTGTTTTTGTTTTTA  
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG  
GCTTAAGAATTTGTCCATTTGCATTCGGAAAAGAATGACCAGCAAAGGTTTACTAATACCTC  
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGTTTCAAGAATTAAAGCTGCAAGAGG  
ACTCCAGGAGCAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTCAATCAAATG  
CCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGTTATTTTA

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**FIGURE 416**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQLLAAYE  
VLSDEKQRKYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGT PRQQDRNIPRGSDI IVDLEVTLEEYAGNF  
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVVCDECPNVKLVNEERTLEVEIEPGVRDGM EYPFI  
GEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLW  
KKGEGLPNFDNNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

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**FIGURE 417**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCACAGCAGGA  
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGGCCAGCCCCGGGGCAG  
**GATG**ACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGTGTTGGGTGGTGTTCATGATCCTGCT  
GATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCTCTAG  
GCCGCACACGGGGCCGCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACGGCCGA  
CTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCC  
CAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA  
CTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAGCGGAGGAG  
CGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTCGA  
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTG  
CTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT  
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGC  
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCCGCCACCTCAT  
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCTTCTCGTGCGCGACCCCTTCGTGCGCCTGAT  
CTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCGCCGTGCC  
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCCGCTCGGCGCGCGAGGCCTTCCGCGC  
TGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT  
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA  
CGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA  
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA  
GGACTGGTTCGCCAAGATCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA  
CTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCCGAGACT**TGA**AAGCTTTCGCGTTG  
CTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCCAGTTTTTTTTATGACCTACGATTT  
TGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT  
TTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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**FIGURE 418**

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSFSPHTGPPLPTPGPDRDRELTAD  
SDVDEFLLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAERRS  
VLRGFCANSSLAFTKERAFFDDIPNSELHSLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSL  
LHRGAPYRDPLRIPREHVHNASAHLTNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI  
SAFRSKFELENEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL  
APFNEHWRQVYRLCHPCQIDYDFVGKLETLEDAQAQLLQVDRQLRFPPSYRNRTASSWEE  
DWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

**Important features:****Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

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**FIGURE 419**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG  
GCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACT  
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA  
AGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA  
ACACCATTGAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAAGATCA  
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTGGGCA  
CGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAATGCCATCG  
TGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTTG  
GGCTGTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT  
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGATCGCAAGACGG  
TTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCACTGTG  
AGGGCACACGGTTACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGGCCAAGGGGC  
TGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT  
TGAGAAATGTAGTTTTCAGCTGTATATGACTGTACACTCAATTTAGAAATAATGAAAATCCAA  
CACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCCAC  
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA  
AGGATGCCTTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGAGACGCCCATGGTGCCCC  
CCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGCTGGTGCTCTACCCTTTCT  
TCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCCTCG  
TCTTCTTTGTGGCCTCCGTGGGAGTTTCGATGGATGATTGGTGTGACGGAATTGACAAGGGCT  
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTTGACTCAGGGAGGTGTCACCAT  
CCGAAGGGAAACCTTGGGGAAGTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA  
AGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT  
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAAATCTTTTTTTCCCATGTGCTTTAGTGGGC  
TTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAGTGTGAACCTTGTTC  
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA  
AGTTCCCCCTTCATCCTTTGGTGCTGAGTTTTCTGTAACCCTTGGTTGCCAGAGATAAAGTGA  
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAATTAAGTGCTTTTCT  
GGGTCAAAAAAAAAA

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**FIGURE 420**

MDLAGLLKSQFLCHLVFCYVFIA SGLIINTIQLEF TLLLWPINKQLFRKINCRLSYCISSQLVM  
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLN HKFEIDFLCGWSLSERFGLLGGSKVLAKKEL  
AYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQH LRDYPEKYFFLIHCEGTRFTEKKHEISM  
QVARAKGLPRLKHHLLPRTKGF AITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKKYHAD  
LYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVNWLFWA  
SLVLYPFFQFLVSMIRSGSSLT LASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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**FIGURE 421**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC  
GCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC  
TGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTCACC  
ACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGGC  
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGGGTGCC  
CTGAAGGAGGAGGTGCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC  
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA  
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACT  
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCGTGCCCCACG  
TCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGACGTGGGCGGCG  
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCTTGGATGAGCAG  
GGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGGGCTGTGCGCCAT  
CTGGGCAAGGTTCAAGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC  
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAAGTGTGTGTCATGATGCTGCACACGGGGCTG  
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACTGC  
TGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTGCTATCCTGGGGGCTGCTCA  
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCTCATCCACCGCTGCTGAG  
TCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCCTGGGCTCTGGGACCTCCA  
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACCTCCACTAGCTCCAAAATCC  
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG  
ACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACTGGAAGCTGTTTTTGCAGCCTGAGG  
AAGCATCAATAAATATTTGAGAAATGAAAAA

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**FIGURE 422**

MDTTRYSKWGSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL  
LDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALREL  
RERVTOGLAEAGRGREDVRTELFRALEAVRLQNNSCEPCPTSWLSFEGSCYFFSVPKTTWAAA  
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFSHWNQ  
GEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:****Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287



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**FIGURE 423**

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGGCTCTCCCGCTTCCTTGAAAAACCCGGCGGGC  
GAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCGGC  
GCCCCAACATGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGATCGC  
GGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGAGCAGAGCCGGGTCCA  
GCCCATGACCGCCTCCAACGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTTTACGC  
CCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAAATGGGAGGCTTTTGCAAAGAATGGTGA  
AATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTGGCCGCTT  
CTTTGTCACCACTCTCCAGCATTTTTTCATGCAAAGGATGGGATATTCCGCCGTTATCGTGG  
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC  
TCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGTCTTTTTTAGCAT  
CTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGAAGTCTTGGAAATCCTGCTTGGTG  
TTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGT  
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAA  
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGA  
TTCAAATGAAGAAGAAAACAAAGACAGCCTTGATAGATGATGAAGAAGAGAAAGAAGATCTTG  
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTGCTGGTGTGGATGAGGA  
GAGAAGTGAGGCCAATGATCAGGGGCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA  
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGCTGACACAGAGGTGGTGA  
AGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTGTAGATTTAATGATGCGT  
TTTCAAGAATACACACCAAACAATATGTGAGCTTCCCTTTGGCCTGCAGTTTGTACCAAATC  
CTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCTCTCTAGTCATTTGGTCTCATG  
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAGAAAAAC  
AAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA  
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCCTAATCAGCACCTTCCAGAGACAAGGCTGC  
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAACGT  
AGAAGCCTTGCATCCTTTTCTTGTGTAAAGTATTTATTTTTGTCAAATTGCAGGAAACATCAG  
GCACCACAGTGCATGAAAAATCTTTCACAGCTAGAAATTGAAAGGGCCTTGGGTATAGAGAGC  
AGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTGTGCTATGTTTTATTTCTTACCTTTAATT  
TTTCCAGCATTTCCACCATGGGCATTGAGGCTCTCCACACTCTTCACTATTATCTCTTGGTCA  
GAGGACTCCAATAACAGCCAGGTTTACATGAACTGTGTTTGTTCATTCTGACCTAAGGGGTTT  
AGATAATCAGTAACCATAACCCCTGAAGCTGTGACTGCCAAACATCTCAAATGAAATGTTGTG  
GCCATCAGAGACTCAAAAGGAAGTAAGGATTTTACAAGACAGATTAAAAAAAATTTGTTTTGT  
CCAAAATATAGTTGTTGTTGATTTTTTTTTTAAGTTTTCTAAGCAATATTTTTCAAGCCAGAAG  
TCCTCTAAGTCTTGCCAGTACAAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTC  
ATCTCAAGGGGTTCCCTGGGTCTTGAAGTACTTTAATAATAACTAAAAAACCACTTCTGATTT  
TCCTTCAGTGATGTGCTTTTGGTGAAAGAATTAATGAAGTCCAGTACCTGAAAGTGAAAGATT  
TGATTTTGTTCATCTTCTGTAATCTTCCAAGAATTATATCTTTGTAAATCTCTCAATACT  
CAATCTACTGTAAGTACCCAGGAGGCTAATTTCTTT

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**FIGURE 424**

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAPW  
CPSCQQT DSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRGPG  
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY  
VFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEEKDDSN  
EEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTREEVEPE  
EAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

**Important features:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide  
isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

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**FIGURE 425**

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG  
CTGGGCCGTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCGCCGCCA  
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA  
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCT  
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
TTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
GATCATTTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG  
AGTGTCAAAATGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA  
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC  
TGCTGTTAATTTCTGGAGAACTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTCACTGCCATGATTTAGCTCC  
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAAT  
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
GACAGGAAATTTGTCAACTCCATACAACTGCTTTTGTGCTGGTATTGGCTGGCTGATCACTTTTTGTTCAA  
AGGAGGAGATTTGTTGACTTCACAGACAGACTCAGGCTTAGTGGCATGTTGTTTCTCACTCATTGGATGCTAA  
AGAAATATATTTGGAAGTAATACATAATCTTCAGATTTTGAAGTACTTTTCGGCAACACACTAGAGGATCGTTT  
GGCTCATCATCGGTGGCTGTTATTTTTTCATTTTGGAAAAAATGAAATTCAAATGATCCTGAGCTGAAAAACT  
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTACTGTTCTCTGCACCAGACATCTGTAGTAA  
TCTGTATGTTTTTCAAGCCTCTCTAGCAGTATTTAAAGGACAAGGAACCAAGAAATATGAAATTCATCATGGAAA  
GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCATGTTACCACGCTTGGACCTCAAAA  
TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCTGGTGTCCACCATGTCGAGCTTTACT  
ACAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCATGA  
GGGACTCTGTAAACATGTATAACATTCAAGCTTATCCAACACAGTGGTATTCAACCAGTCCAACATTTCATGAGTA  
TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
ACCCACCACCTTCAACGAAGTAGTTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCATTCCTCGTG  
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAAGATGGCCCGGACATTAAGTGGACTGATCAACGTGGG  
CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATAACCTGAGATAAGATTTTT  
TCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATCCCTGAGAAT  
CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGTGAAAAAGTTCTACAAGG  
GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT  
CTTGCTAGGATGATTAAAGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA  
AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTATTTCTACGAAGAGCAAAGAGAAATTTCAAGAAGAGCA  
GATAAATACAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGAACTCTCCGAAATCAAGGCAA  
GAGGAATAAGGATGAACTTGATAAATGTTGAAGATGAAGAAAAAGTTAAAGAAATCTGACAGATGACATCAG  
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGACAGTTGTACTGCCA  
GAATTATCTACAGCACTGGTGTAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGCGCGTTTATAAATATTTTA  
GACTTTCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT  
TTTAAACACCTTTAAAAAATATTAAACGATTTCTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCACTCCATG  
GACCATAGATTGCTGTCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTGGCTGACCTGAAAAGAGGTA  
TAGTTTTTGGTCACTTGTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTCTTTTTAAAAACACCCAT  
GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTCTCTCA  
AAGGTTGAAAAATGCTTTTAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA  
TAGCAATTAAGTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
TGTGTTTCATGATTTTTCTGAAATTTGCTTTTATAGAAATTTTCCACTGATAGTTGATTTTTGAGGCATCTAATAT  
TTACATATTTGCCCTTCTGAACCTTGTGTTTACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTGG  
TTTTTCACTCCTGTCCAGTCTATTTATTTCAATAGGAAAAATTTACTTTACAGGTTGTTTTACTGTAGCTTAT  
AATGATACTGTAGTTATTCAGTTACTAGTTTACTGTGAGGGCTGCCTTTTTTCAAGATAAATATTGACATAATA  
ACTGAAGTTATTTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTTGTAG  
CTCAAGAATCACAATTTGTGAGTAACTGTAGTTGTTTATGTTTATTAATTCAGAGTGTACAGAATGGTAAAAAT  
CCAATCAGTCAAAAGAGGTCAATGAATTAAGGCTTGCAACTTTTTCAAAAAA

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**FIGURE 426**

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTQDFYSLLGVSKTASSREIRQAFKKLALKLH  
PDKNPNPNNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGIYD  
DDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD  
RMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTA  
FAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR  
LAHHRWLLFFHFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSPLYVFQPSLAVFK  
GQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFANDKEPWLVDFFAPWCPPCRALL  
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHSAEQILEFI  
EDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGS  
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLGFLPQVSTDLT  
PQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDCQAYAQTCQKAG  
IRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRNKDEL

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

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**FIGURE 427**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGCA  
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTTGA  
GTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGGTAG  
CGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACGCGTTCTCAATT  
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG  
TCAGCGCCGCGCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACAACCTACC  
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC  
GCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATGC  
GTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTTCTGATCAAA  
ATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT  
TGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG  
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT  
CCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT  
CTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGA  
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGAGACACTTAAACCAGCT  
ATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC  
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCGAATAACACCTTCCA  
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTGTGATTGCAGTAAATTACT  
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAACTTTTAATTATTTTTCT  
AAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTTTGTACACATTGATTGTTAT  
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTTCAGCTTATAGTTCTTAAAAG  
CATAACCCCTTACCCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTTGGAATGACAAAT  
GATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG  
CTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGAAATAAAATTTAACATTTAAAAAA  
AAAAAA

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**FIGURE 428**

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPLGGAAGHPGSAVSAA  
PGILYPGGNKYQTIIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRHAM  
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEGSVC  
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLScriQKdHH  
QASNSSRLHTCQRH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

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**FIGURE 429**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCCC  
TTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTACGGACCC  
CAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT  
CCTGGTAACTTGGGTTTTTACTCCTGTAACAAGTAAATAACAAGTCTTGCTACAGAGAATAT  
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGTGCTTT  
CAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATTTCCAAA  
TGAAAATCAAGTAGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA  
CAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATA  
CAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAGTGACCCCAT  
TCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAAATATCATTGG  
ATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA  
TGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAAACCGGAAAGATATAGTGGCGA  
CAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC  
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTTGTCGAGAAATAAC  
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAA  
AGAAGATACAGAAAGTTTAGAAATATTCAGAAATGAAGTAGCTCGGCAATTAATAAGTGAAAA  
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA  
GAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTG  
AGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCGTATTTGACTTACATTCTGG  
AAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACCTGATACAGCCCCAGGAGAGCAAGC  
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATATAG  
GTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAACTTGAAAAACAGTTTGTAAGCCTTTC  
AACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTATATTTTCATAATTCTATGTGTAT  
TTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 430**

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQM  
LHPIFEEASDVKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQ  
RSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILHDDC  
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREITFEN  
GEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP  
ADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV  
ASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:****Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66



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**FIGURE 431**

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGCA  
GGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG  
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGCGTG  
GACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG  
CGGGGTTGCGGTTCTGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGCTTCTG  
GCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG  
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTGCTACAGC  
TGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGTGAGCTGCTACAAC  
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG  
ACTGTGTCCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA  
GGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGC  
AACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCTCCAGAGCCCACG  
ACTGTGGCCTCAACCACATCTGTCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC  
ACCAAACCCATGCCAGCGCCAACCAAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCC  
CGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGG  
CAGTATCCTGCAAAAGGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCACAGCT  
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTGAGCTTCTCCACCTGGA  
AATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCTGTTCCCA  
CCACTGGACTGGGCTGGCCAGCCCCCTGTTTTTCCAACATTCCCAGTATCCCCAGCTTCTGC  
TGCGCTGGTTTTCGGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA  
GCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCTCTTGTGATG  
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC  
TACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAATGGCTCCCC  
ACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC  
TTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGGTACCCAATTCGCCCTATAGTGAGTCGTA

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**FIGURE 432**

MDPARKAGAQAAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSFNKMKTVKCAPGVDVCTE  
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQAQDRCNAKLNLTSRALDP  
AGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKCFDGNVTLTAAANVTVSLP  
VRGCVQDEFCTR DGVTGPGFTLSGCCQGSRCNSDLRNKTYFSPIPLVRLPPPEPTTVAST  
TSVTTSTSAPVRPTSTTKPMPAPTSQTPRQVEHEASRDEEPRLTGGAAGHQDRSNSGQYPAK  
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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**FIGURE 433**

CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCCATGGGAGTT  
GGTGCTGGTCTTCTCTGCAGCCTGCTGGCCCCCATGGTCTTGCCAGTGCAGCTGAAAAGGA  
GAAGGAAATGGACCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTTCGC  
TGTGGTCTCTTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTTTCAA  
TCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCAGGTGGAGAACCTCATCACCGCCAATGC  
AACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG  
GCGGCTGCTTGAACCTTTGGATGCAAAATGTCGATGCTTAAGAAAACCGGCCACTTCAGCAACA  
GCCCTTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCTATCCCCTCTAACACCATT  
CCTCCACCTGATGATGCAACTAACACTTGCCTCCCCACTGCAGCCTGCGGTCTGCCACCTC  
CCGTGATGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTGGTCTTTGTGG  
CTACTTGTTTGTGGATGGTATTGTGTTTGTTAGTGAAGTGTGGACTCGCTTCCCAGGCAGGG  
GCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCCGTGGCCCTCCATCACCTTCTGCTCCTA  
GGAGGCTGCTTGTTGCCCGAGACCAGCCCCCTCCCCTGATTTAGGGATGCGTAGGGTAAGAGC  
ACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCACTTTGTCATCATTTCT  
TCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTTATCCCACCTGATCCCAGTCT  
GAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCCCAGCGTTGACGTCAGG  
CAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCACGAGGAGTCCCCATCTGCC  
CCGCCCCCTTACAGAGCGCCCCGGGGATTCCAGGCCCAGGGCTTCTACTCTGCCCTTGGGGAAT  
GTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGGGACCCTACCCCTTCCAACC  
TTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAGATGCAGACTACAGTCCCTGC  
AATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCCGTTGGGGCCAGCACACCGGGA  
TGGATGGAGGGAGAGCAGAGGCCCTTGGCTTCTCTGCCTACGTCCCCTTAGATGGGCAGCAGAG  
GCAACTCCCGCATCCTTTGCTCTGCCTGTCGGTGGTCAGAGCGGTGAGCGAGGTGGGTGGAG  
ACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAGGTTGAAGGTATAACGAGAGTGGG  
AACTCAACCCAGATCCCGCCCCCTCCTGTCTCTGTGTTCCCGCGGAAACCAACCAAACCGTGC  
GCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTATCCTCAACAACAACAGAAAAAAGGAAT  
AAAATATCCTTTGTTTCCT

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**FIGURE 434**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSVGILLILSRCKC  
SFNQKPRAPGDDEEAQVENLITANATEPQKQRTevQPSGGSLWNLRRLLEPLDANVDA

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**FIGURE 435**

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC  
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA  
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT  
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA  
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
AGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA  
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG  
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA  
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA  
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA  
GTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCACAGCCACCACCC  
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT  
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC  
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT  
CATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCTTTTGCCAACAATTTTA  
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA  
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTCTTTTGTGGAAAA  
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG  
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT  
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA  
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

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**FIGURE 436**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFH  
YDCGNKTVTPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD  
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

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**FIGURE 437**

GTTCCTCTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAGCTCTTGTGGCAGG  
TAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTACCTCACGGCGCAAGTGTGGATTCTGT  
GTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCCAGAACTGCCCCCTCCGTTTGCTCGTGAGTAACCAAGTTCA  
GCAAGGTGGTGTGCACGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACC  
TCATGGAGAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGTTGG  
GCAGGAATCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAACACCCTGGAGCTGTTCCG  
ACAACTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACA  
ACCCCATCGAAAGCATCCCCTCTTACGCCCTCAACCGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCA  
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAAGTTGGGCATGTGCA  
ACATTAAAGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTG  
AGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTGAAGTACAGGTCAGCCTGA  
TTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAGTCAACTTGGCCACAATAACCTCTCTTCTTTC  
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCCCTGGAAGTGTGATTGTG  
ACATTCTGTGGCTAGCCTGGTGGCTTCGAGAGTATATACCCACCAATCCACCTGCTGTGGCCGCTGTCATGCTC  
CCATGCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCTTCATCATGG  
ACGCACCTCGAGACCTCAACATTTCTGAGGGTGGATGGCAGAACTTAAGTGTGCGACTCCCCCTATGCTCTCCG  
TGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGCCTCCCGCCACCAAGGATCTCTGTCTCAACGACG  
GCACCTTGAAGTTTCCACGTGCTGCTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCA  
ACTCCAACGCCTCGGCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAAGTACAGCTTCTTACCACAG  
TAACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTACCACGTCCACTG  
GTTACCAGCCGGCATATACCACCTTACCACGGTGTCTATTGAGACTACCCGTGTGCCCAAGCAGGTGGCAGTAC  
CCGCGACAGACACCACTGACAAGATGCAGACCAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT  
GCTTTGTGGCAGTGACTCTGCTAGCTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGC  
GGAGTACAGTCACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGCAG  
CAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTATGACCATATTAAGT  
ACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGCCTGGGGAAGTCTCTGCACCCACAGTCA  
CCACTATCTCTGAACCTTATATAATTAGACCCATACCAAGGACAAGGTACAGGAACTCAAATATGACTCCCCCT  
CCCCCAAAAAGTATAAAATGCAATAGAATGCACACAAGACAGCAACTTTTGTACAGAGTGGGGGAGAGACTTT  
TTCTTGATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAACAGATTATATTAAGTTTAAAGACAAAA  
AGTCAAAACA

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**FIGURE 438**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTR  
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN  
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE  
GAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEELEMMSGNHFPFIRPGSFHGLSSLKKLWVMNS  
QVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDCDILWLAWWL  
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP  
MSSVKWLLPNGTVLSHASRHPRI SVLNDGTLNF SHVLLSDTGVYTCMVTNVAGNSNASAYLNV  
STAE LNTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQTTRVPKQV  
AVPATD TTDKMQTS LDEV MKTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVE  
IIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHW TENS LGNSLHPT  
VTTISEPYIIQTHTKDKVQETQI



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**FIGURE 439**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCA**ATG**AGGCTG  
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC  
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA  
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC  
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAA**ATAG**TGAAAAAT  
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACCCTGATC  
TTCATAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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**FIGURE 440**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEVK  
HCTDQISFKRSLKKSWWK

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**FIGURE 441**

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG  
GGGTTGCTGGTTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC  
ACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG  
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG  
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA  
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCAGGAAGATGGAGGTCAAGCAGAAGGGGC  
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT  
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC  
CAAAGAGGCCCCAGCCGACAAGTGATCGCCACAAGCCTTACTCACCTCTCTAAGTTTAGA  
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG  
AGGCGAATAAATGTTCAAACCTGTA

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**FIGURE 442**

MPSPGTVCSSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG  
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 443**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG  
TGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGTTT  
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTGCTC  
CTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT  
ATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAAGCTGCTCATCTTACA  
CCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTTGTCCCC  
CGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAAGGGCAA  
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAATCACGCCG  
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGAGACAATGGA  
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAACAC  
AAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCACTAACCAACAAGTGAAG  
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTCAATCATGTTGCT  
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAACCTGTGTTGGAAGTAACAACAACCTCC  
CTGCTCCTGGCACCAGCCGTTTTGGTTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG  
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGACACGGGCAGCAGAGTG  
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA  
GAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCTGCCTGCAG  
TTGTGGCAAGAAGCCCCAGCTCAGAATGAACACACCCCAAGAGCCTCCTTGTTTCATAACC  
ACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGATGTTTTTAAACACACACCTC  
TAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC  
AATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

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**FIGURE 444**

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGWV  
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ  
QEAELTPRPAGVVPGA

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**FIGURE 445**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTGC  
TGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAAGA  
GGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACCTGG  
TGTCACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG  
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCTGTGGA  
TGTCACAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCCGTATCC  
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTACCATGCAGG  
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCTGTGCGCCGCCGCCTCTGCC  
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT  
GCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGACCATCCTCCT  
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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**FIGURE 446**

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE  
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCLGC  
VNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.



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**FIGURE 447**

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAGA  
TGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT  
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC  
CCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTGGATG  
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGACCGGT  
TCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAGAACCAG  
GGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC  
TGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA  
TGGAGAAGGCTTCCCTCCCCCTCCCCTCCCCTTGGGGCTTTGTGGCAAAAATCCTATGGTTATCC  
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCTACTAACAGAC  
TTGCTACTCACTGGGAACCCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTGCTGTTTCCTCT  
GTCCTGTCAGGTCTCCTGGGGATGGTGGCCCACATGATGTATTACAAAGTCTTCCAAGCGACT  
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAATTATGGCTGGGCCTTCTACATG  
GCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCACCACCTTCAACACGTACACCAGG  
ATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAACCCGAACCTGCCTACCA  
CATCACCATCAGTGTTCCTCGGCGGCTGTCAAGTGCAGCCCCCACCCTGGGTCCCTTTGACC  
AGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC  
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA  
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT  
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTA  
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCCTAAGGGATTCTGGGTGCCA  
CTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCACCCACATCTCACACATCCAGAA  
TTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGCTAAACCATGGAGATAAAAAGAAG  
AGTAAATAACACTTCCCGACCTTAAGGATCTGAAA

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**FIGURE 448**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV  
SLDGDNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKRGE  
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQLP  
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTCLELWL  
LLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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**FIGURE 449**

[illegible]

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**FIGURE 450**

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN  
LSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQIT  
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIQDCRSLKF  
LDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIVVSSL  
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITLAGNL  
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSGHLLSAV  
TNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLI  
VVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVII  
NEYGSCTCHQQPARECEV

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**FIGURE 451**

TTGAGCGCAGGTGAGCTCCTGCGCGTTCGGGGGCGTTCCCTCCAGTCACCCTCCCGCCGTTAC  
CCGCGGCGCGCCCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGA  
CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT  
ACCATCCATAGCCAGATAGATTATCTTACACTGAACTGATCAAGTACTTTGAAAATGACTTCG  
AAATTTATCTTGCTGTCCTTCATACTTGCTGCACTGAGTCTTTCAACCACCTTTCTCTCCAA  
CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA  
GTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAAT  
GTTTTTATTACAAAACCTACCCTAACCATTTTGGTAACTGGCCTCTTGCAGAGAAT  
CATGGGATTGTTGCAAATGATATGTTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCAC  
ATGAATATTTTATGATTCCAAGTTTGGGAAGAAGCGACACCAATATGGATCACAACAGAGG  
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGAACAGATGTAAAAATACATAAGCGCTTT  
CCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAGAGTTGCCAAAATTGTT  
GAATGGTTTACGTCAAAGAGCCCATAAACTCTTGGTCTTCTCTATTGGGAAGACCCTGATGAC  
ATGGGCCACCATTGGGACCTGACAGTCCGCTCATGGGCGCTGTCATTTAGATATTGACAAG  
AAGTTAGGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATC  
ATCACAAGTGATCATGGAATGACGCGAGTCTGAGGAAAGGTTAATAGAAGTTGACCAGTAC  
CTGGATAAAGACCCTATACCCTGATTGATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAA  
GGTAAATTTGATGAAGTCTATGAAGCACTAACTCAGCTCATCCTAATCTTACTGTTTACAAA  
AAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCACCAATCATAGCA  
GTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACCAC  
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTATAGCCCATGGTCTGCCTTCAGA  
AAGAATTTCTCAAAAAGAAGCCATGAACTCCACAGATTTGTACCCACTACTATGCCACCTCCTC  
AATATCACTGCCATGCCACACAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCA  
ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTTAAACCAGCA  
GAATATGACCAAGAGGGGTCATACCCTTATTTATAGGGGTCTCTCTTGGCAGCATTATAGTG  
ATTGTATTTTTTTGTAATTTTCATTAAGCATTTAATTCACAGTCAAATACCTGCCTTACAAGAT  
ATGCATGCTGAAAATAGCTCAACCATTATTACAAGCCTAAATGTTACTTTGAAGTGGATTTGCAT  
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATTCTGGGAAACCAGTT  
CCAAACATCTGCAGAAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACA  
CACATACACACACACGGACCAAATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGT  
CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTGGCGCAGAT  
AATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATATATTGCACTTTAAATTTCT  
CTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAACTTGATTG  
AAAATGACAACCTTTTGCACCCATGTCACAGAATACTTGTTACGCATTGTTCAAACCTGAAGGA  
AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAA  
GGTGATAAGTGTGAAAATTAAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATTCC  
CAACAGCAGAATGCACTGTGGGCATTTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCA  
TTTATTTTTTCCCTCAAAAGAGAGTCAAATACTGACAGATTGCTTCTAAATATATTGTTTCTGT  
CATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCATAATAATGAAGACAC  
CATGAATATACTTTTCTTCTATATAGTTCAGCAATGGCCTGAATAGAAGCAACCAGGCACCAT  
CTCAGCAATGTTTTCTTGTGTTGTAATTATTGCTCCTTTGAAAATTAAATCACTATTAATT  
ACATTAAAAATCAAATTGGATAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 452**

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ  
VTNVFITKTPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIWIT  
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED  
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITS DHGMTQCSEERLIEL  
DQYLDKDHYT LIDQSPVAAILPKEGKFDEVYEALTAHPNLT VYKKEDVPERWHYKYN SRIQP  
IIA VADEGWHILQNKSDDFLLGNHGYDNALADMHP IFLAHGPAFRKNFSKEAMNSTDLYPLLC  
HLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPHYGVSLGS  
IIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Important features:****Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,  
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

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**FIGURE 453**

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC  
**TATG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTGCT  
GATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGACCAA  
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA  
TGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGGCAGGC  
TGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAAACCTCCA  
ATATGAGGACAAGTTCCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCAACACCTA  
CACATCTCAGGATCTCAAGAGTGCCTGGCAAAATTCAAGGAGGGGGCAGAGATGGAGAGTTT  
AAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGAGGAACTGAA  
GAAAGACTTTGATGAGCTGAATGTTGTCAATTGAGACTGACATGCAGATCATGGTACGGCTGAT  
CAACAAGTTCAATAGTTCCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTCTTTGATCTTGA  
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGTGGT  
GATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGTTTGTGCTGGGCGC  
TGCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT  
GCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGTCCTGTTTGCCTGTG  
CTCCCTGCTGCGCCACTTCCCCATGCCCAGCGGCAGTTCTGAAGCTCGGGGGGCTGCAGGT  
CCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTGCGCGTGGTCACACTGCT  
CTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGAGCTGACCCAGGAGATGTC  
CCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAGGCCTGTGGGAACAGGGCTG  
GTGCGAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGATGCCCGTGAGAAGGTGCTGCA  
GACACTGGGCGTCCTCCTGACCACCTGCCGGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG  
GACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCAGCCTGGAGCTGCAGGATGGTGA  
GGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAACAGCTTGCTGAAGGAGCTGAGAT**AG**  
**AGG**CCCCACACCAGGACTGGACTGGGATGCCGCTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG  
GGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCTTGGCCATTAAATGGAAACCTGAAGG  
CCAA  
AA

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**FIGURE 454**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEEELD  
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLOYEDKFRNNLKGKRLDINTNTY  
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI  
NKFNSSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAAFVLGA  
AFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKLGGLQV  
LRTLVEKGTQTEVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPEKLQYRQVHLLPGLWEQGW  
CEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE  
DEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340



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**FIGURE 455**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAGT  
GGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCCTA  
CCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT  
CTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC  
TCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGTCCTTG  
TGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCCCCTGGA  
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTTCTCGCCA  
ACAATGATGTTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG  
GAGCTGGGGCCGGGGAAGACGCCCCGGTCGGATGACAGCAGCAGCCGCATCATCAATGGATCCG  
ACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACT  
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAGGAAGAAAGTTT  
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAAGTTTATGAATCTGGGCAGCAGATGTTCC  
AGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCTAACGACCTCATGC  
TCATCAAATGAACAGAAGAATTCGTCCCCTAAAGATGTCAGACCCATCAACGTCTCCTCTC  
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCCAAG  
TGCACTTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG  
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT  
CCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCT  
GGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTCA  
CCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTTGAGTCATCCCAGGACTCAGCACACCGG  
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTCCCAGAGA  
TGTTGAGAATGTTTCATCTCTCCAGCCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC  
CCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGGGAACAATTTCCAAAAGTGTCCAG  
GGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTT  
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAATAAAAAA

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**FIGURE 456**

MATARPPWMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS  
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPV  
YESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPSAGTKCLVSG  
WGTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCN  
GSLQGLVSWG DYPCARPNRPGVYTNLCKFTKWIQETIQANS

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**FIGURE 457**

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTTGCTTCCTGAACT  
AGCTCACAGTAGCCCGGGGGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGCAGG  
CCAAGTACAGCAGCAGAGGGACATGCTGGATGATGATGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG  
CCACAACCTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA  
CCCTGCTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACCAGC  
TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTC  
TTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCGTGAGCTGTATAACA  
AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATA  
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAAC  
AAGAAGACCTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCC  
CTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCATATTATAATAGATG  
TCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAGAATTGA  
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG  
AAGGTGACTTGAATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAG  
ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTTCCTCGTGTTCCTGTT  
CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCAC  
CAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAA  
TGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGAATAAGAACTTTTGAAGTAGAGGAAA  
TACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTAC  
CAGCAAATACACAAGGAATTCCTTTTGTGTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC  
CATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCATTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
GCATTCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATAT  
ATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGT  
GAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCATTTTCTTCCATTGACCCATATTTATACCTTTCAGGT  
ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

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**FIGURE 458**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY  
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL  
KRCVCERRAGMVKPESLHVPPETLGEGD

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**FIGURE 459**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCAC  
TGGCGGCCCCGCAACACTCCGTCTCACCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCTGT  
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGTGGT  
CAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA  
GTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAGGATGA  
GAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA  
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC  
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAACCT  
ACTTTGCGTTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGTGCTTTGAAG  
ACCGCATGATCATGAGTCCTGTGAAAACAATGTGGGCAGAGGCCTAAACATCGCCCTGGTGA  
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC  
ACCTAGTGAAATTCCTTAAAGAAATTCCGGGGGGTGCCTGGTGTGGTGGCCTCCTACGACG  
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTGGGGAGTTCCTACG  
CAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA  
GCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACGAGGGATGGCCAGAGC  
TGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCCTCAG  
CCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA  
GGAGCAGGGGGTGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGACGCTGTGTGCGCCTCTCCTC  
CTCGGAAACAGAACCTCCCACAGCACATCCTACCCGGAAGACCAGCCTCAGAGGGTCCTTCT  
GGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGGAAGCTGCTGACGGCTGGTCCTG  
AGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTATTTTGTGCTGGTTTTGAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 460**

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA  
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV  
MHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKDLRG  
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop) .**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

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**FIGURE 461**

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA  
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCCTC  
TAGAACCCGACCCACCACCATGAGGTCCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGGCGT  
CCAGTGGTCCTTGCTTCTGGCTGTCCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTATTAA  
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA  
GTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA  
GCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCACCGGAGA  
CAGAGGAAAGGAGGCCAACCAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCACACAGCACA  
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGAGG  
GCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA  
GACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTCAGAGAA  
GCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCCAAAGTCAGCACAGAATGCT  
GGTCCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC  
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTTCCAGAGCCCCACGACGCA  
GAGAAACCAAAGACTGAAGGCCGCAACTTCAAATCTGAGCCTCGGTGGGATTTTGAGGAAAA  
ATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAAGCCTC  
CAAGTCGCTGTGGCTCCAGAACTCTTCTGCCCAACCTCACTCTCTTCTGGACTCCAGACA  
CTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTGCACCACCTTTGGCTTCATGGAGCT  
CAACTACTCCTTGGTGCAGAAGGTCTGACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT  
CCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGTGCCGTGGTGGGCAACGGGGG  
CATCTGAACAACTCCCACATGGGGCCAGGATAGACAGTCACGACTACGTGTTCCGATTGAG  
CGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGACTCGGACATCCTTCTACGGCTTTAC  
CGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAAGCTGCCTCT  
TGGGAAGGACGTCCGCTACTTGCACTTCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC  
ACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTTTCTGGTTCAGGCACAGACCCAGGA  
AGCTTTTTCGGGAAGCCCTGCACATGGACAGGTACCTGTTGCTGCACCCAGACTTTCTCCGATA  
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGATGGTGCCCACTGGAGGATATACCGCCC  
CACCAGTGGGGCCCTCCTGCTGCTCACTGCCCTTCACTCTGTGACCAGGTGAGTGCTTATGG  
CTTCATCACTGAGGGCCATGAGCGCTTTTCTGATCACTACTATGATACATCATGGAAGCGGCT  
GATCTTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACACGATGA  
AGGGATAATCCGGCTGTACCAGCGTCCTGGTCCCGGAACTGCCAAAGCCAAGAATTGACCGGG  
GCCAGGGCTGCCATGGTCTCCTTGCTGCTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC  
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTTCAAGGAGTTCCAAGGGAACAC  
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCA  
GTACATTGCTGTAGGTCTGAGGCCAGGGATTTTTAATTAAATGGGGTGATGGGTGGCCAATA  
CCACAATTCTGCTGAAAAACACTCTTCCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCC  
TGGATTTACAGAAACATATAGATCTGGTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCT  
TGAAGGTATTACTTAACCTCACTACAGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC  
TAGAAGGGTCTATACTTGTCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAAAC  
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAAA  
AAAAAAA

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**FIGURE 462**

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK  
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS  
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQNGGQTRKLTASRTVSEKHQGKAA  
TTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPKKKPQATPPPAPFQSPTTQRNQRLK  
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW  
DRLEHFAPPFQFMELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNNGGILNNSH  
MGQEIDSHDYVFRSLGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVPLGKDVRV  
LHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHHPDFLRVMKNRFL  
RSKTL'DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSWKRLIFYINH  
DFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

**Important features:****Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463



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**FIGURE 463**

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCGCAAGGGTGAGGGCGGCCCCAGAAC  
CCCAGGTAGGTAGAGCAAGAAGATGGTGTTTCTGCCCCTCAAATGGTCCCTTGCAACCATGTC  
ATTTCTACTTTCTCTACTGTTGGCTCTCTTAAGTGTGTCCACTCCTTCATGGTGTGAGAGCAC  
TGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCCTTGGAATAAAATACGACTTCCTGA  
GTACGTCATCCCAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACCTTCTG  
GGGAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCATAGTCA  
CCACCTGCAGATATCTAGGGCCACCCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACC  
CCTGCAGGTCTTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAGCCCCCTCCT  
TGTCGGGCTCCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTTCGGGAGACTTTCCACGG  
ATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGAAGTACTAGCATCAACACAATT  
TGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTCAAAGCAAGTTT  
CTCAATCAAAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCCATTGGTGAAATC  
TGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGTGATGTCACTGTGAAGATGAGCACCTA  
TCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGAGCAAGATAACCAAGAGTGGAGTCAA  
GGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGCACTGGATGCTGCGGT  
GACTCTTCTAGAATTTTATGAGGATTATTTGAGCATACCGTATCCCTACCCAAACAAGATCT  
TGCTGCTATTTCCCGACTTTCAGTCTGGTGCTATGGAAAAGTGGGACTGACAACATATAGAGA  
ATCTGCTCTGTTGTTTATGTCAGAAAAGTCTTCTGCATCAAGTAAGCTTGGCATCACAGTGAC  
TGTGGCCCATGAAGTGGCCACCAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGAAATGA  
TCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTGTCTGTGAGTGTGACCCATCC  
TGAAGTGAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGACGCAATGGAGGTAGATGCTTTT  
AAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTGCTCAGATCCGGGAGATGTTTGA  
TGATGTTTCTTATGATAAGGGAGCTTGTATTCTGAATATGCTAAGGGAGTATCTTAGCGCTGA  
CGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCATAGCTATAAAAAATACAAAAACGA  
GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT  
TTGCTCTAGAAGTCAACATTCATCTTCATCCTCACATTTGGCATCAGGAAGGGGTGGATGTGAA  
AACCATGATGAACACTTGGACACTGCAGAGGGGTTTTCCCTAATAACCATCACAGTGAGGGG  
GAGGAATGTACACATGAAGCAAGAGCACTACATGAAGGGCTCTGACGGCGCCCCGGACACTGG  
GTACCTGTGGCATGTTCCATTGACATTCATCACAGCAAATCCAACATGGTCCATCGATTTTT  
GCTAAAAACAAAACAGATGTGCTCATCTCCAGAAAGAGGTGGAATGGATCAAATTTAATGT  
GGGCATGAATGGCTATTACATTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT  
TTTAAAAGGAACACACACAGCAGTCAGCAGTAATGATCGGGCAAGTCTCATTAACAATGCATT  
TCAGCTCGTCAGCATTGGGAAGCTGTCCATTGAAAAGGCCTTGGATTTATCCCTGTACTTGAA  
ACATGAAACTGAAATTATGCCCGTGTTCAGGTTTGAATGAGCTGATTCCATGTATAAGTT  
AATGGAGAAAAGAGATATGAATGAAGTGGAACCTCAATTCAAGGCCTTCCTCATCAGGCTGCT  
AAGGGACCTCATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG  
GAGTGAACACTACTCTCGCCTGTGTGCACAACATATCAGCCGTGCGTACAGAGGGCAGAAGG  
CTATTTTCAGAAAGTGAAGGAATCCAATGGAACTTGAGCCTGCCTGTGACGTGACCTTGGC  
AGTGTGTTGCTGTGGGGGCCAGAGCACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTT  
TTCTTTGTCCAGTACTGAGAAAAGCCAAATTGAATTTGCCCTCTGCAGAACCCAAAATAAGGA  
AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAATAAAAACCTCAGGAGTTTCC  
ACAAATTCTTACACTCATTGGCAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAG  
GAAAACTGGAACAACTTGTACAAAAGTTTGAAGTGGCTCATCTTCCATAGCCCACATGGT  
AATGGGTACAACAAATCAATTCTCCACAAGAACCGGCTTGAAGAGGTAAAAGGATTCTTCAG  
CTCTTTTGAAGAAAATGGTTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATGAAAGA  
AAACATCGGTTGGATGGATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAGAGCT  
TGAACGTATGTAAAAATTCCTCCCTTGCCCGGTTCCCTGTTATCTCTAATCACCACATTTTGT  
TGAGTGTATTTTCAAAGTAGAGATGGCTGTTTTGGCTCCAAGTGGAGATACTTTTTTCCCTTC  
AACTCATTTTTTGAATATCCCTGTGAAAAGAATAGCTGTTAGTTTTTCATGAATGGGCTTTTT  
CATGAATGGGCTATCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGCTAAACC  
CAAGTGTGGGTTCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 464**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY  
DLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP  
PQEQIALLAPEPLLVLGYPTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM  
AFPCFDEPAFKASFSEIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS  
DFESVSKITKSGVKVSVYAVPDKINQADYALDAVTLLEFYEDYFSIPYPLPKQDLAAIPDFQ  
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELHQWFGNLVTMEWWNDLWLNELF  
AKFMEFVSVSVTHPELVGDFYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG  
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDFGCSRSQHS  
SSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPDTGYLWHVPL  
TFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTLGLLKGTHTA  
VSSNDRASLINNAFQLVSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMKRDMDN  
EVETQFKAFILRLRLDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE  
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALCRTQNKEKLQWLLD  
ESFKGDKIKTQEFPPQILTILGRNPVGYPPLAWQFLRKNWNKLVQKFELGSSSIAHMVMGTTNQF  
STRTRLEEVKGFFSSSLKENGSQLRCVQQTITETIEENIGWMDKNFDKIRVWLQSEKLERM

**Important features:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360

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**FIGURE 465**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACT  
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGA  
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACAC  
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGCTGCACGGAGGC  
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA  
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC  
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG  
TCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCT  
CAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG  
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCTGGGTATGACTGAGAACTGCAATAG  
GAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAACTTGGCTCAAGA  
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGAC  
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT  
TGGGGCTCAAATTTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTC  
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA  
CTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC  
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA  
TGATGGGTACATTTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGT  
GGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA  
GAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC  
TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTC  
CTGCTTAACTCTATTACCCCCACGATTCTTACCGCTGCTGACCACCCACACTCAACCTCCCTC  
TGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCCATTCGTCCATGAATCATCTT  
CCCCACACACAATCATTATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC  
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC  
CCTGTCCTTTCA

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**FIGURE 466**

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLIE  
SGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDEFNNLVNSLPLWAPQPPA  
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCNLLN  
GTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLID  
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQ  
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS  
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVCPSC

**FIGURE 467**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTG  
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGGCCCTTCG  
AGGAGCTTCTGCATTGCTGGTCTGTTCCCTGCAGCTTTTCTGCCCCCGCCGAGTGTAACCA  
GGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGGAAAA  
ATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCCAAGAGTTCTCAAAAAATATATCTGT  
CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTTGGCACT  
GAGAGTTGAACGTGCCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGGCTGACGAGT  
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAA  
GATCCGGACTCTGCTGAATGCAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAT  
AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAA  
GGTGTACTTATTAATTGGATCCAGAAAACAACACTGTTTGGGAATTTGCAAACATACGGGCATT  
CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTCCTGGCAGGGAAC  
AGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTTCTAATGAGATAAT  
CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCAGGAGGGGTAGCCCG  
AGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT  
CTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTCTCTACAAAGATTGAGCCGGG  
CACACTGGGAGTGGAGCATTATGGGATACCCCATGCAGAAGCCAGGATGCTGAAGCCTCAT  
CCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCGCATCAC  
CTGCATCTATGATCCACTGGGCATATCAGTGAGGAGGACTTGCCCACTTGTCTTCCCCAA  
GAGACCAAGAAGTCACTCCATGATCTATTACAACCCAGAGATGAAGCAGCTCTATGCCTGGAA  
TGAAGGAAACCAGATCATTTACAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAAATGCAT  
TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC  
CCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATACGT  
ATGCCTCCTTTCCCAAATGTCATGCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC  
ATCAGGAAAGTTTTCAACAATGTCCATTACTCCCCCAAACCTCCTGGCTCTCAAGGATGACCAC  
ATTCTGATACAGCCTACTTCAAGCCTTTTGTTTTACTGCTCCCCAGCATTTACTGTAACCTCTG  
CCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCCCTAATATTCACCACCTGGCTTTTCTC  
TCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTCAAATGTCTATTGATATCTCCCAATTT  
CACTGCCCAACTAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTGTAGACAAGGT  
CTCACTATGTTGCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT  
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAAATACTATTTCTTATTG  
AGGTTTTAACCTCTATTTCCCTTAGCCCTGTCTTCCACTAAGCTTGGTAGATGTAATAATAAA  
GTGAAAATATTAACATTTGAATATCGCTTTCAGGTGTGGAGTGTGTCACATCATTGAATTC  
TCGTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGT  
AACACAATTACAAAGTGAAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTTCCATTG  
CCCAAGGAAGCATCAAATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTT  
TCAGCCTAAAAATAATAGTCTGTCCCTTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAAT  
AGGCCTTTCAAATGATAATTTCTCCAGAAAACCAAGTCTAAGGGTGAGGACCCCAACTCTAGCC  
TCCTCTTGTCTGTGTCCTCTGTTTCTCTCTTTCTGCTTTAAATTCATAAAAGTGACACTG  
AGCAAAAAAAAAAAAAAAAAA

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**FIGURE 468**

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQEF  
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE  
AEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTVWEF  
ANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL  
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKIEPGTLGVEHSWDTPCRSQ  
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK  
QLYAWNEGNQIIYKLQTKRKLPLK

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**FIGURE 469**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC  
AGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC  
CTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGG  
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCTGGGG  
CGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCAAGCAC  
CACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTACCGCTGC  
TCCATGGACTTGAAGAACATCAATTTTTTAGGGCGCTTGCCTGGTCTCAGGATACCCACCATCCT  
TTTCCTGAGCACAGCCTGGATTTTTTATTCTGCCATGAAACCCAGCTCCCATGACTCTCCAG  
TCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA  
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGGCTGTGGTGTG  
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA  
GGACATTCCCCCTCCCCTCCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTGCCCTCTCCCCA  
CATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGTGCATTGCTCAGAG  
TCCCAGGTCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT  
AGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT  
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC  
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA  
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCACTGAAGCCCCCA  
ATTCCCACAGCTTTTCCATTAAAATGCAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT  
ATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCAAGGATCAGCCCTGAGAGCAG  
GTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGC  
AGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGGCAACTACACACCAACATGCTGG  
CTTTAGAATAAAAGCACCAACTGAAAAA

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**FIGURE 470**

MRGATRVSIMLLLVTYSDCAVITGACERDVQCGAGTCCAI SLWLRGLRMCTPLGREGEETCHPG  
SHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Important feratures:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52



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**FIGURE 471**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTCC  
TCCAGGACCCAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTG  
CTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGGGCC  
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAA  
AGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCCTCT  
GTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCC  
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG  
GAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTA  
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAGGCTTCTCTG  
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTTCGTGGTGGGATCAGGAAAGCAGG  
GCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGG  
AAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGATTGTGTGAAACTG  
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTCATGGGATGTATTGTTTCCACTCGTG  
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA  
TATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA  
CTAATGAGGATTATTAAGCTAAAACCTGGGAATAGGAGGCTTAAATTGACTGCCAGGCTGG  
GTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG  
GTCGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAA  
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAA  
TCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG  
GGTGA CTGAGACTCTAACTAA

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**FIGURE 472**

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT  
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP  
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFVVG  
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 473**

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTTT  
TGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTGGT  
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC  
AAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC  
CAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT  
AATTCTTGGTGTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA  
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA  
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT  
TTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT  
TTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAAATGCGATACA  
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA  
TGTTGCCAAGGAAAAA

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**FIGURE 474**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG  
IVKGRNLDSRGLILGAEAWGRGVKKNT



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**FIGURE 476**

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRVI  
VVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRILHK  
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMALNQ  
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALRAHSC  
LSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVLKA  
DVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFR RPFWREEHIEGGSNTDR  
PSRMIFYPPPREGALLLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV  
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHG WVETAVKSALRAAIKI  
NSRKG PASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQNTTHTRTSH

**Important features:****Signal peptide:**

amino acids 1-21

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**FIGURE 477**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT  
GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA  
GAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCTCT  
GCTGCTGTTCCACAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCACTTCCGACCCCGCGTTGATCTGCAT  
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA  
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGTTTCCAGAAGAACAATGACCTAACAAGTTGCTG  
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG  
ATATAGAAAACCAAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTT  
CTGTCTCTTGCAATAAGGTTATAAATCATCACCAGACCACTTGTGCGCATCTTGTCTCAGAATAGGCCAGAGTG  
GATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC  
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT  
AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTGTATGATGACCTGAA  
GCAAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAAGAGCACTTCAG  
AAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG  
AGCCATGATAACCCATCAAAATATTGTTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATGTACAGGCTGTTGTGTA  
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
CACATTGTTTTCCCGCGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCTT  
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACTGGAGC  
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGACGAATGGGATGTGAGGTGTATGAAGCTTATGGTCA  
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGGTACGTTGGGGTGCCCTGGC  
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAATACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCTGAGAAGACACAGGAAGCCCTGGACAGTGTGGCTG  
GCTTCACACAGGAGACATTGGTCGCTGGCTCCCGAATGGAACCTCTGAAGATCATCGACCGTAAAAAGAACATTTT  
CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAAGTGTACA  
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCCTGACACAGATGTACTTCCCTC  
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT  
AGAAGACTTGCAGAAAATTTGGGAAAGAAAGTGGCCTTAAACTTTTGAACAGGTCAAAGCCATTTTCTTCTATCC  
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT  
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG  
TGCACTGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTTGTTTTGCCTTTCTCCTATTTTTTTTTTAACC  
TGTTAAACTCTAAAGCCATAGCTTTTGTGTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAAATAAATCA  
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA  
GATCCCAGTTTATGTTCTGTGCTTCTCATGATTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
CAAAGGGACCTCTGTGCCTTCTTCTTTGTTTTGTGATAAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA  
TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATCTGAAAACTGCTTACAATTTCATGTTTTCTAGCCACTCCAC  
AAACCACTAAAATTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
CTGCGTAAATTAATTTGTGTAAGGGAAGGTTGATCATACCAACATTTCTTAACTCTCTAGTTAGATA  
TCTGACTTGGGAGTATTAATAATTTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA  
CAGTAGGAACCTGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
GGTGGGCCCACTGAACTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCCTGAACTGGGAACAAAGATCT  
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCCTTGATT  
AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC  
TATTACAGATAAAAAA

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**FIGURE 478**

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFNF  
LFSPLPTPALICILTFGAIFLWLITRPQPVLPDLLNQQSVGIEGGARKGVSQKNNDLTSCC  
FSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ  
FVGIFAQNRPEWIISELACYTYSMAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG  
NVEKGFTPSLVKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC  
FTSGTTGDPKGAMITHQNIVSNAAAFLLKCEHAYEPTPDDVAISYLPLAHMFERIVQAVVYSC  
GARVGFFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE  
LQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAAPMSTSVMTFFRAAMGCQVYEAYGQTEC  
TGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNÝFTVNNEGEVCIKGTNVFKGYLKDPEKT  
QEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVH  
GESLRSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKIGKESGLKTFEQ  
VKAIFLHPEPFSIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622



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**FIGURE 479**

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGGCCGAGCGGGGC  
CCGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC  
GGT**ATG**GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC  
TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCTAGACA  
GGGGCCGTGCTTTTCTGCTGGTGAAGTGTCAATATCAAGTTGATCCTGGACACTCGG  
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC  
CGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGACGTAGAGGTGTAT  
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGTGAGGATGAGGCCCGG  
GAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGCCACGTGATGGCAAAA  
CGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTCTTCTCAACATGGTA  
GCGCCCGGCCGAGTGTCTGCACTGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA  
GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA  
TGGGCCTTCTGTTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTCTAAGTCACCTGCC  
CTCTCTTCTGGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG  
GCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGCTTCTGCAGCAAAGTT  
GAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGAGTTCAGCCCTGACCCA  
CTCCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCAATTGCAGGGAACCGACCCAATTAC  
CTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCTCCTCAGATGATAACAGTT  
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTTGGTCTGAGGGGCATC  
CAGCATACTCCATCAGCATCAAGAATGCCCCGTGTCTCAGCACTACAAGGCCAGCCTCACT  
GCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTTCTGGAAGAGGACCTGGACATT  
GCTGTGGATTTTTTCAGTTTCTGAGCCAATCCATCCACCTACTGGAGGAGGATGACACCTG  
TACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG  
TACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTCAGGAGGTCTTGTACAGGAGGAG  
CTTGAGCCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCT  
GAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACGTTTCCCGATCCTACCCTTTGGCATC  
GTCGGCCTCAACATGAATGGCTACTTTACGAGGCCTACTTCAAGAAGCACAAGTTCAACACG  
GTTCCAGGTGTCCAGCTCAGGAATGTGGCAGTCTGAAGAAAGAAGCTTATGAAGTGGAAGTT  
CACAGGTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC  
CTGCCAGACACAGAGGGCCACACCTACGTGGCCTTTATTTCGAATGGAGAAAGATGATGACTTC  
ACCACCTGGACCCAGCTTGCCAAGTGCCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT  
CGGGGCCCTGTGGAGATTGTTTTCGGAAGAAGAACCCTTCTGCTGGTGGTGGGGTCCCGGCTTCC  
CCCTACTCAGTGAAGAAGCCACCCTCAGTCACCCCAATTTTCTGGAGCCACCCCCAAAGGAG  
GAGGGAGCCCCAGGAGCCCCAGAACAGACAT**AG**AGACCTCCTCCAGGACCTGCGGGGCTGGGT  
ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTA  
GGGGCTGGGGCTACCTTGTTTTTAACATGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCC  
CTGCTCCAACACCCCGTTCTGAGTTAAAGTCTATTTATTTACTTCTTGTGGAGAAGGGC  
AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGCCCTTGAATACCCTCAC  
TTTCCAGGCCTGGCTCAGAATCTAACCTATTTATTTGACTGTCCTGAGGGCCTTGAACACAGGC  
CGAACCTGGAGGGCCTGGATTTCTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC  
TTACTCAGGAACTGCTGTGCCCAACCCATGGACAGGCCCTCCTCTCAGCCTTCTCTTTGTCCAGA  
AGACTCACTCAGAGACCCTTAGACACTGGACAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGA  
TTTCCAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAA  
AAAAAAAAAAAAAAAAA

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**FIGURE 480**

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVVNIKLILDTRR  
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEARE  
QGRGIHVIVLNQATGHVMAKRVDFTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLKDTA  
KALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSSAEEA  
ECHWADTELNRRRRRFCSKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGNRPNYL  
YRMLRSLLSAQGVSPQMITVFIDGYEPMDVVALFGLRGIQHTPISIKNARVSQHYKASLTA  
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLY  
RVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVSRSYHFGIV  
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKEAYEVEVHRLLEAEVLDHSKNPCEDSFL  
PDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVVRGNHRGLWRLFRKKNHFLVVGVPASP  
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

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**FIGURE 481**

GAAAGAATGTTGTGGCTGCTCTTTTTCTGGTGA CTGCCATTCATGCTGAACTCTGTCAACCA  
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT  
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTT  
CCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCA  
TTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCA  
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAA ACTCTGGAA  
TTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT  
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC  
TGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA  
AACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTA  
ATGATGCCTTCATTGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC  
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT  
CATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAG  
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAA  
AATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAA  
GCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACTTCAAAGACCTAAGGAAAA  
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT  
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA  
AATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCA  
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT  
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 482**

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN  
REATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFL  
KIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLILSGIWQRRRKNKEPSEVDDAEDKCENM  
ITIENGIPSDPLDMKGGILMMPS

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**FIGURE 483**

CGTCTCTGCGTTGCGCCATGCGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC  
CCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGTGT  
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCACCCG  
GGCCGAGTGCTGTGCCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA  
CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCTACTGCCTTCCCTGCAAAGATTTCGTGCGA  
CGGCGTGAGTGCGGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGCTGCGAGTG  
CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA  
CCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGCGTCATGTA  
CCGGGGCCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTCGTGCGTCGT  
GGACCAGACGGGCGAGCGCCACTGCGTGGTGTGTGAGCGGCGCCCTGCCCTGTGCCCTCCAG  
CCCCGGCCAGGAGCTTTGCGGCAACAACAACGTCACCTACATCTCCTCGTGCCACATGCGCCA  
GGCCACCTGCTTCTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCC  
TGAGGAGCCGCCAGGTGGTGTGAGTCTGCAGAAGAGGAAGAGAACTTCGTGTGAGCCTGCAGGAC  
AGGCCTGGGCCTGGTGCCCGAGGCCCCCATCATCCCCTGTTATTTATTGCCACAGCAGAGTC  
TAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGACCACCTTGGGGATCCAGAACC  
TCCCTGACGATATCCTGGAAGGACTGAGGAAGGAGGCCTGGGGGCCGGCTGGTGGGTGGGAT  
AGACCTGCGTTCCGGACACTGAGCGCCTGATTAGGGCCCTTCTCTAGGATGCCCCAGCCCC  
ACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCTATTAA  
TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGACTGC  
TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA  
GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT  
GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT  
AGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT  
GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG  
GGTGTGTACGGAGGGTCTAGTCTGAGTGCCTGTGGGGACCTCAGAACACTGTGACCTTAGCCC  
AGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGCCACCATTCCCTGCCAGCCCAAGA  
CCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGTCCTGTGAAGGCCATTGAGAAATGCCCA  
GTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC  
CACCCAGCGTCTCCCTGCTGCTGTCCACGTCAGTTCATGAGGCAACGTCGCGTGGTCTCAGA  
CGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGGCGGAGCCAAAGTCCACTCTG  
GGGGAGCTCTGGCGGGGACCACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACG  
CCAAGACTCACGCATGTGTGACATCCGGAGTCTGGAGCCGGGTGTCCAGTGGCACCCTAG  
GTGCCTGCTGCCTCCACAGTGGGGTTCACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCC  
GGCCAGGCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG  
GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACGACGGCTCACCTCCCCCTCCAT  
CTGCGTTGATGCTCAGAAATCGCCTACCTGTGCTGCGTGTAACACAGCCTCAGACCAGCTA  
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGC  
TTGGGCATCCTCCTCCAGCCTCCTCCAGCCCCAGGCAGTGCCTTACCTGTGGTGCCAGAAA  
AGTGCCCTAGGTTGGTGGGTCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCC  
CTGCCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAA

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**FIGURE 484**

MRPGAPGPLWPLPWGALAWAVGVSSMSGSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC  
CA  
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPDCS  
GLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCEHVVCPRPQSCVVDQTGS  
AHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG  
GESAEEEENFV

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 73-77, 215-219

**Osteonectin domain proteins.**

amino acids 97-130, 169-202

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**FIGURE 485**

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCCC  
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGA  
AACGGGCGTTCGAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATCATC  
GTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGATCATG  
GAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGAAGAAC  
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC  
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAATAACATC  
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC  
GGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC  
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA  
ATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAAC  
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG  
CCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAAACAGCAAGTCCCAGACACCA  
GCCCCAGTTCGGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAAACCAATGAG  
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG  
GTGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACC  
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA  
GACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGGAAGGGAGAAAC  
CAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA  
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG  
AAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTGAATTGAA  
CTGGAATCACATATTTTACAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA  
ATACTGAAAACCTGTGAAATGTACTAAATAAAATGTACATCTGA

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**FIGURE 486**

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGAV  
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT  
LQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD  
LSENNQRRQLQALSEPQPRLOAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCRQVEK  
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRVPVGGRGFGGAGELGQTPQVQAALSVSQENPEM  
EGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF  
NVEDQKRDTINLLDQREKRNHTL

**Important features:****Signal peptide:**

amino acids 1-29



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**FIGURE 487**

AACTCAAACCTCTCTCTGCGGAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGG  
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCCATGTAT  
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCT  
ATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG  
TTAAAATGCACCTTTCTCCAGCTTTGCCCCCTGTGGGTGATGCTCTAACAGTGACCTGGAATTTT  
CGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCC  
ATGAGTGGGCGGTTTAAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC  
ATCCTTCTCTGGAACCTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCCA  
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT  
GAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT  
GTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG  
GAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA  
GACACAGACTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATT  
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTTCCAACCAAGTTC  
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT  
CACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAA  
GTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAAGACACTACTTACAGTGT  
TATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTACATTT  
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC  
TTCCCACATTCTCAATTTAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAACAGTAAATC  
CTAAATTCAAACCTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACCTATGAGACACATC  
TTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATTTTTGTCTG

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**FIGURE 488**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW  
NFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK  
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFFQHYRKKRWAERAHK  
VVEIKSKEEERLNQEKKVSYLEDTD

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**FIGURE 489**

[illegible]

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**FIGURE 490**

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINFM  
KTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF  
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNWLRLK  
EAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP  
VDIYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIYSSDHG  
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPLPQNLSG  
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGASILPQLFD  
LSSDPDELTNAVVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQYNSNVIA  
NLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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**FIGURE 491**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA  
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGC  
CTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT  
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGT  
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA  
CATCTATAGCACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCAGGCCATGATGGTGAC  
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT  
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGG  
AGGCCTCCTGGGATTTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC  
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTT  
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGAGAAATCG  
CTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG  
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAAC  
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA  
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG  
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA  
GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC  
AACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT  
TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAA  
AGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT  
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC  
TGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG  
AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA  
GGCAGCCTGGGACATTTAAAAAATA

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**FIGURE 492**

MASLGLQLVG YILG LLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ  
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFI  
LGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR  
NRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

**Important features:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

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**FIGURE 493**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT  
TATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAGAA  
CCATGGCTGTGCCAGCCGGCAGCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC  
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCACCTTC  
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTGTGAAG  
CTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC  
AGAAGACGTTTTCCCTGAGAAGACATAGAAAGAAAATCAACTTTCACCTAAGGCATCTCAGAAA  
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATGATGCAGCT  
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA  
GGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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**FIGURE 494**

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSET  
RQCGPPCTFWPCFELCCLDSFGLTNDVFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Important features:**

**Signal peptide:**

amino acids 1-25



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**FIGURE 495**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT  
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA  
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTTGCT  
ATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGAGTCT  
GCTTTGAGCAGTGCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGACTCAG  
CCCGGACCTCGGATGACAGGCTTTGTCGCAGTGTCAGCTAATGGAACATCAGGGGAACGATGA  
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGATCTGGGA  
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCTTCATTCTGTGACC  
TGTCTGAGGCCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAGAATTCTGGA  
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGATGACCCCTATG  
GCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCCTTCTGTGAGATT  
TTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA  
CTTTATAAATGAAAA

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**FIGURE 496**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTFYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL  
ARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLLCRSVS

**Important features:**

**Signal peptide:**

amino acids 1-24

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**FIGURE 497**

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACTC  
CTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCCTCCTGGC  
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCCTCA  
GAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG  
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA  
GGAGACTTCAAACCTTCGGATTTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT  
GGTCTTCTCTCATTGTCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC  
GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAAGGCCCTGAAGCCCACCAAGCCGGGCT  
CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAGTGGGCCTCTC  
ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC  
CAAGGTATTTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCACAGGCCAAAAG  
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTCCCAAAGTGTGATGAGAT  
TAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGAAATGGTTGACCCC  
ATTTGACCCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTACAAGACCATTAAGGT  
GCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAATTTTCGTTGTCTATGT  
CCTCAAAGTGCCTACCAAGGAAATGCCACCATGCTGGTGGTCCTCATGGAGAAAATGGGTGA  
CCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA  
AACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCAGAAGTATGAGATGCATGA  
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCCTTTGCTGACCTTAGTGAACCTCTC  
AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA  
AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAAGTCTTATTCATGCCTCCTGT  
CATCAAAGTGGACCGGCCATTTTCATTTTCATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT  
TCTGGGCAGGGTGGTGAATCCGACTCTCCTATAAATTCAGGACATGCATAAGCACTTCGTGCTG  
TAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGATACCAGCAATGGATGGCAGGGGAG  
AGTGTTTCCTTTTGTTCTTAAGTAGTTAGGGTGTCTCAAATAAATACAGTAGTCCCCACTTA  
TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT  
TATATATATTTTTTCTACACATACATACCTATGATAAAGTTTAATTTATAAATTAGGCACAG  
TAAGAGATTAACAATAATAACAACATTAAGTAAAATGAGTTACTTGAACGCAAGCACTGCAAT  
ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA  
CAGTGTGGAGACATTGGGCAAGGGGAGAATTACATCCTGGGTGGGACAGAGCAGGACGATGC  
AAGATTCCATCCCCTACTCAGAAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTTCTGG  
AATTTTTTCATTTAATGTTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA  
AACCATGGATAAGGGAGGACTACTACAAAAGCATTAATTTGATACATATTTTTTAAAAAAA  
AAAAAAA

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**FIGURE 498**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E E  
E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I K R  
G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F D T E  
C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P V F T E  
V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L A L E D Y  
L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A T G R N L Q  
V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F L G R V V N P  
T L L

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**FIGURE 499**

[illegible]

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**FIGURE 500**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLAT  
LQEAATTQENVAVWRKNWMVGGEGGASGRSP

**Important features:**

**Signal peptide:**

amino acids 1-18

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**FIGURE 501**

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCCTCGGGCTTGAGGGGAAGAG  
GCTGACTGTACGTTCTTCTACTCTGGCACCCTCTCCAGGCTGCCATGGGGCCCAGCACCCC  
TCTCCTCATCTTGTTCTTTTGTTCATGGTCGGGACCCCTCCAAGGACAGCAGCACCACTTGT  
GGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCCAGTGCCAGGACCAGAG  
TAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAGGTGGC  
AGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGATCGTCT  
GGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTGTAGAGTTTGATGA  
GAAGGTGACTGGAGGCCCTGGGACCAAGGCAAGGGAAGAAGGAATGAGAAGTACGATATGGT  
GACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCGATTTGGTGG  
CCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACGTGTTAGATGG  
GACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTTGCCATGGCTGC  
CCGGAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCAGCTGGTATATGG  
TGGCTTTCTTTATTTTGCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTGGTGAGATGGAGAA  
CACTTTGCAGCTAATCAAATTCACCTGGCAAACCGAACAGTGGTGGACAGCTCAGTATTCCC  
AGCAGAGGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACATCGACCTGGTAGCTGA  
TGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGCACTTGTGTCTGGCCAA  
GTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCATGTCCCAGAGAGAATGC  
TGAGGCTGCCTTTGTTCATCTGTGGGACCCTCTATGTGCTCTATAACACCCGTCCTGCCAGTCG  
GGCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCCCTGAACGGGCAGCACTCCC  
TTATTTTCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTATAACCCCCGAGAACGCCAGCT  
CTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGAGATGAGGAAGAAAGAGGAGGA  
GGTTTGAGGAGCTAGCCTTGTTTTTTGCATCTTTCTCACTCCCATACATTTATATTATATCCC  
CACTAAATTTCTTGTTCTCATTCTTCAAATGTGGGCCAGTTGTGGCTCAAATCCTCTATATT  
TTTAGCCAATGGCAATCAAATTCTTTAGCTCCTTTGTTTCATACGGAACCTCCAGATCCTGAG  
TAATCCTTTTAGAGCCCGAAGAGTCAAACCCCTCAATGTTCCCTCCTGCTCTCCTGCCCCATG  
TCAACAAATTTAGGCTAAGGATGCCCCAGACCCAGGGCTCTAACCTTGTATGCGGGCAGGCC  
CAGGGAGCAGGCAGCAGTGTTCTTCCCCTCAGAGTGACTTGGGGAGGGAGAAATAGGAGGAGA  
CGTCCAGCTCTGTCTCTCTTCTCACTCCTCCCTTCAGTGCTCTGAGGAACAGGACTTTCTC  
CACATTGTTTTGTATTGCAACATTTTGCATTAAAAGGAAAATCCACAAAAA  
AAA

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**FIGURE 502**

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALERLAQCQDQSSRHAAELRDFKNKML  
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETONPALPCVEFDEKVTGGPGTKGKGRRN  
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF  
TLAMAARKASRVVPFPWVG TGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLANRTVV  
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDEQQWDTP  
CPRENAEAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN  
PRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251



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**FIGURE 503**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT  
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCC  
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA  
CGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCTCTCAGCA  
CGGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGGGTGTT  
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC  
CATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT  
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTT  
CCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG  
AGTGCTGCGTCCCCAGTAGGGATGGCGCCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC  
ACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

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## **FIGURE 504**

MGGLLLAAFLALVSVPRQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTL  
TPENNLRTLSSQHGLGGCDQSVMDLIKRN'SGWVFENPSIGVLELWVLATNFRDYAIIFTQLEF  
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Important features:**

**Signal peptide:**

amino acids 1-20

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**FIGURE 505**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA  
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC  
CTGCTTGCTCTGGCAACAGGGCTTGTTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAGTGC  
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGGGGCG  
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACATAGTT  
CACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG  
TCCTTCCCCCACCCTGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG  
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCTCTCA  
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCAG  
TTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAG  
AACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG  
GACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATC  
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA  
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCA  
TCACCCTCCATTTCCACTTGGTGTGTTGGTTCTGTTCCTGTTCACTCTGTTAATAAGAAACCCTAAGCC  
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC  
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTG  
GGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT  
ATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 506**

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC  
LKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV  
RPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLR CANITII EHQKCENAYPGNITDTMVCA  
SVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:****Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

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**FIGURE 507**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAGG  
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA  
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC  
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCCTGTC  
CAGAAGCCGAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCATCCTT  
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCCGAGCCC  
GACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCCCCGGTTG  
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC  
CCCCAGTAGGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGGCTGTTGGGA  
CTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 508**

MRRLLLVTSLVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVLF  
PVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEERP  
RLWVMPNHQVLLGPEEDQDHIYHPQ

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**FIGURE 509**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC  
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGGACTCGGCGCGCGAGGTGCTTGGGCGCG  
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCGGCCCATGAAAGCGCAGCCATG  
GCGGCATCTGAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG  
ACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA  
ACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCGGCATCT  
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC  
AAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC  
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCATTCTGAAGCA  
AAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTT  
TTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTCGGTATCGAACC  
ATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT  
GCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCTCTTTTTGAAAATA  
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG  
TAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT  
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCTGGGGTGGGGGCATTGG  
TCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAATGCCATCTGGGCATACA  
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTGTAGCTCACATAAAGAACTT  
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA  
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAAACTGTAGTAGTT  
GGTCTAGAAACAAAATACTCC

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**FIGURE 510**

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDHT  
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQNTS  
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIGCKM  
YYSRRGIRYRTIDEHDAII



**FIGURE 511**

GACTTTTGCTTGAATGTTTACATTTTCTGCTCGCTGTCCCTACATATCACAAATATAGTGTTCCAGCTTTTGGTTAAACAA  
TTTGGGGTGTGAGGAGTTGAGCTTGCTCAGCAAGCCAGCATGGGCTAGGATGAGCTTTGTTATAGCAGCTTGCCAA  
TTGGTGCTGGGCCTACTAATGACTTCATTAACCGAGTCTTCCATACAGAATAGTGAGTGTCACAACCTTTGCGTA  
TGTGAAATTCGTCCCTGGTTTACCCACAGTCAACTTACAGAGAAGCCACCAGTGTGATTGCAATGACCTCCGC  
TTAACAAGGATTCCCAGTAACCTCTCTAGTGACACACAAGTGCTTCTCTTACAGAGCAATAACATCGCGAAGACT  
GTGGATGAGCTGCAGCAGCTTTTCAACTTGACTGAACTAGATTTCTCCCAAAACAACCTTTACTAACATTAAAGGAG  
GTCGGGCTGGCAAACCTAACCCAGCTCACAACGCTGCATTTGGAGGAAAATCAGATTACCGAGATGACTGATTAC  
TGTCTACAAGACCTCAGCAACCTTCAAGAAGTCTACATCAACCACAACCAATTAGCACTATTTCTGCTCATGCT  
TTTGCAGGCTTAAAAATCTATTAAGGCTCCACCTGAACTCCAACAAATTGAAAGTTATTGATAGTCGCTGGTTT  
GATTCTACACCCAACCTGGAAATTCTCATGATCGGAGAAAACCTGTGATTGGAATTCTGGATATGAACTTCAAA  
CCCCTCGCAAAATTTGAGAAGCTTAGTTTTGGCAGGAATGTATCTCACTGATATTCCTGGAATGCTTTTGGTGGGT  
CTGGATAGCCTTGAGAGCCTGTCTTTTATGATAACAACTGGTTAAAGTCCCTCAACTTGCCCTGCAAAAAGTT  
CCAAATTTGAAATTCTTAGACCTCAACAAAAACCCATTCAACAAATCCAAGAAGGGGACTTCAAAAATATGCTT  
CGGTTAAAAAGAACTGGGAATCAACAATATGGGCGAGCTCGTTTCTGTGCGACCGCTATGCCCTGGATAACTTGCCT  
GAACTCACAAAGCTGGAAGCCACCAATAACCTTAACTCTCTTACATCCACCGCTTGGCTTTCCGAAGTGTCCCT  
GCTCTGGAAGCTTGATGCTGAACAACAATGCCTTGAATGCCATTTACCAAAAGACAGTCGAATCCCTCCCCAAT  
CTGCGTGAGATCAGTATCCATAGCAATCCCTCAGGTGTGACTGTGTGATCCACTGGATTAACTCCAACAAAACC  
AACATCCGCTTCATGGAGCCCCTGTCCATGTTCTGTGCCATGCCGCCCCGAATATAAAGGGCACCAGGTGAAGGAA  
GTTTTAATCCAGGATTCGAGTGAACAGTGCCTCCCAATGATATCTCAGCAGAGCTTCCCAATCGTTTTAAACGTG  
GATATCGGCACGACGGTTTTCTAGACTGTGAGCCATGGCTGAGCCAGAACCTGAAATTTACTGGGTCACTCCC  
ATTGGAATAAGATAACTGTGGAACCCCTTTCAGATAAATACAAGCTAAGTAGCGAAGGTACCTTGGAAATATCT  
AACATACAAATTGAAGACTCAGGAAGATACACATGTGTTGCCCAGAATGTCCAAGGGGCAGACACTCGGGTGGCA  
ACAATTAAGGTTAACGGGACCCCTTCGGATGGTACCCAGGTGCTAAAAATATACGTCAAGCAGACAGAATCCCAT  
TCCATCTTAGTGTCTTGAAAGTTAATTCCAATGTCATGACGTCAAACCTAAATGGTGTCTGCCACCATGAAG  
ATTGATAACCCCTCACATAACATATACTGCCAGGGTCCAGTCGATGTCCATGAATACAACCTAACGCATCTGCAG  
CCTTCCACAGATTATGAAGTGTGTCTCACAGTGTCCAATATTATCAGCAGACTCAAAAGTCATGCGTAAATGTC  
ACAACCAAAAATGCCGCCCTTCGCAGTGGACATCTCTGATCAAGAAACCAGTACAGCCCTTGCTGCAGTAATGGGG  
TCTATGTTTGCCGTATTAGCCTTGCGTCCATTGCTGTGTACTTTGCCAAAAGATTTAAGAGAAAAAATAACCAC  
CACTCATTAaaaaAGTATATGCAAAAACCTTTCAATCCCACTAAATGAGCTGTACCCACCACTCATTAACTC  
TGGGAAGGTGACAGCGAGAAAGACAAAGATGGTTCTGCAGACACCAAGCCAACCCAGGTGACACATCCAGAAGC  
TATTACATGTGGTTAACTCAGAGGATATTTTGCTTCTGGTAGTAAGGAGCACAAAGACGTTTTTTGCTTTATTCTGC  
AAAAGTGAACAAGTTGAAGACTTTTGTATTTTGACTTTTGCTAGTTTGTGGCAGAGTGGAGAGGACGGGTGGATA  
TTTCAAATTTTTTTAGTATAGCGTATCGCAAGGGTTTGACACGGCTGCCAGCGACTCTAGGCTTCCAGTCTGTGT  
TTGGTTTTTATTCTTATCATTATTATGATTGTTATTATATTATTATTTTATTTAGTTGTTGTGCTAAACTCAAT  
AATGCTGTTCTAACTACAGTGCTCAATAAAATGATTAATGACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 512**

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL  
TRIPSNLSSDTQVLLLQSNNAKTVDLQQLFNLTELDQSNNFTNIKEVGLANLTQLTTLHL  
EENQITEMTDYCLQDLNLQELYINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS  
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV  
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDYALDNLPELT  
KLEATNNPKLSYIHLAFRSVPALESMLNNAALNAIYQKTVESLPNLREISHSNPLRCDCV  
IHWINSNKTNIRFMEPLSMFCAMPPEYKGHVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT  
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV  
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPH  
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETST  
ALAAVMGSMFAVISLASIAVYFAKRFRKKNYHSLKKYMQKTSSIPLNELYPPLINLWEGDSE  
KDKDGSADTKPTQVDTSRSYYMW

**Important features:****Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 508-530

**N-glycosylation sites:**Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;  
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

**N-myristoylation sites:**

Amino acids 16-22;224-230;464-470;637-643;698-704

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**FIGURE 513**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC  
CAGCAATATGCATCTTGACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT  
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT  
GAGCAATGCAGAGAGAGAGGTTGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC  
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA  
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA  
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG  
ACAGGCCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG  
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT  
GGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGAAGGAGCTGCAGAATGC  
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG  
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA  
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG  
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG  
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA  
CTTGATACACCA

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**FIGURE 514**

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR  
EVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHVNNAAAGQA  
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN  
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

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**FIGURE 515**

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT  
TTCCCTCCGACGCGCCACGGCTGCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCGAA  
CCCCTCCGCGGAGAGGAGCGAGGCGGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG  
AAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG  
CCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCGGTGTG  
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGGTTCGCCG  
GCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCCGCTGCTACCCCTGCGCCCGC  
TGCGAGCCCGGCGTCCGGCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTGGCGGGCGG  
GCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCCCGCCCGCCGG  
GACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCTCT  
GGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCA  
GGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGGCCCCGGGGCGGGT  
GAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACTGGAAGAGCAAGAG  
CGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCAGGG  
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACACCCCGCAGGCGGAAGC  
CCTGGCCGCGAGCCGCCAGGACGCGATTGGCCCGGAAGTTCGCGCCACGCCCGAGCCACCCGA  
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAGAGCGGCTTCGTGTACGC  
GATCGGGGAGAAGTTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCTGTGCACCGAGGAGGGGCC  
GCTGTGCGCGCAGCCCGAGTGCCCCGAGGCTGCACCCGCGCTGCATCCACGTGACACGAGCCA  
GTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCCGGGGCAAGACCTATCAGAC  
TTTGGAGGAGTTCTGTGGTGTCTCCATGCGAGAGGTGTGCTGTGAAGCCAACGGTGAGGTGCT  
ATGCACAGTGTACGCGTGTCCCCAGACGGAGTGTGTGGACCCTGTGTACGAGCCTGATCAGTG  
CTGTCCCATCTGCAAAAATGGTCCAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG  
AGAAGTGAAGACTGACGAGTGCACCAATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT  
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCAGAACACA  
AACTCTGACTTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAAGTATC  
AGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTTCCTTTTCTTGATA  
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA  
AATCCTTCTCTAAATAAATGTGCTATTTTACAGTAAGTACACAAAAGTACACTATTATATAT  
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTTTCTATAGATGCAGAT  
TAAAAATGCTGTGTGTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 516**

MPSSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNELG  
RPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALAAA  
AQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKEKFAPGPSACPCLCTEEGPLCAQ  
PECPR LHPRCIHVDT SQCCPQCKERNYCEFRGKTYQTLEEFVVS PCERCRC EANGEVLCTVS  
ACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYE EGTWRIERQA  
MCTRHECRQM

**Important features:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

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**FIGURE 517**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT  
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC  
GGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC  
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG  
TTTTAGAGAACC TAGTACGAAGTGTTCCTCTGGGGAGCCAGGTCGTGAGAAAAATCTAACT  
CTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTACACATG  
GAGACGCTTCAACTGAGAATGATGTTTAAACCAATCCTATCAGTGAAGAACTACAACCTTTC  
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCCATTCCTGGT  
CGATCAAACCAAACAATGTTTCCATTGTTTGCATGCAGAGGAACCTTATATTGAAAATGAAG  
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATGTTGCCAGTTG  
TTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCACCACTTTAGATA  
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCTCAGGTGAAACTG  
CGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA  
AAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGACACCAGCAACCCAG  
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG  
CAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA  
ATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTCTAGATCTAAACTCTATG  
AATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA  
CATTAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTAAAAGTTTATTAAACAATAA  
TATAAAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGATTTAAGCAAAGTGCATTTTT  
TCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTATAAAAAATTTTTCTATTGTAGT  
TCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACAATTTTCATATGCACTAAAAACC  
TAATTTAAAAATAAAATTTTGGTTCAGGAAAAAA

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**FIGURE 518**

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPKH  
VYSIASKGSKFKELVTHGDASTENDVLNPISEETTTFTPTGGFTPEIGKKKHTSTPFWSIKP  
NNVSIVLHAEOPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDKSTG  
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNPAYRE  
DIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD  
IKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Important features:****Signal peptide:**

amino acids 1-19



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**FIGURE 519**

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTG  
GATTTGAAAGTTGAGAGCAGCATGTTTTTGGCCACTGAAACTCATCCTGCTGCCAGTGTTACTG  
GATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGT  
GATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC  
TGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC  
AGTGTGCCCTATTGGGCGCTTCCAGAACC GCGTACACTTGATGGGGGACATCTTATGCAATGAT  
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC  
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC  
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAGAA  
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA  
TTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAG  
AATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTG  
AGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAA  
ACCATTGTGCTGCATGTGAGCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG  
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG  
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCT  
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTT  
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA  
GAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG  
AGGTCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA  
GCCTTTTTGAGAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGT  
GTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTCCCAGCTGTCTCCTGTCTCATT  
GTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA  
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG  
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTTGGATCAGACCCTCCTGTGGGCAGGG  
TTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAACCCAAATCAA

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**FIGURE 520**

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGE  
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV  
FKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL  
RMSVEYSQSWGHEFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIVLHVS  
PEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPV LILIVKKT CGNKSSVNSTVLVKNT  
KKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRSDRNNS  
LEKKSGGGMPKTQQAF

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**FIGURE 521**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG  
TTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA  
ACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCAGGA  
TGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTGGCCC  
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT  
TGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGATGAGAA  
TGAAAATCGCACAGGAACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAACA  
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAACTGGAGATA  
TTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAGTAAGCAGTA  
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA  
AGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA  
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGATGGAAAAGGAAA  
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA  
TTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT  
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA  
GCTGAAAAAAAAAAAAAA

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**FIGURE 522**

MQDEDEGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYLQ  
DENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWEES  
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEDG  
KGNMNCAYFHNGKMHPTECNKHILMCERKAGMTKVDQLP

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**FIGURE 523**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGC  
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA  
GAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAAT  
TGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA  
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG  
AACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA  
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT  
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTT  
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA  
AAATTCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT  
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGA  
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG  
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA  
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA  
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG  
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAACCTGGTGGGTGGCCCGCATGCTGGGGAGGGT  
CTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATATAATAAATGCATGCTATT  
CAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG  
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAA

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**FIGURE 524**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPKKAYD  
MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQI  
KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWINPT  
LISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG  
IEFDPMLDERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

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**FIGURE 525**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTC  
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA  
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT  
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACCGAGA  
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCATGGAC  
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC  
TTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT  
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT  
TAACACGTCAATAAAAAAATAATCTCCCAGA

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## **FIGURE 526**

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE  
CHLCTESLKSNQGRVQFLHDGSC

**Important features:**

**Signal peptide:**

amino acids 1-19



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**FIGURE 527**

CGACG**ATG**CTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGG  
CTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCT  
CGTCGCTCAGCCCCCTATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGT  
CGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC  
TGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCTGAGGC  
AGCTGCACGGGTTGCTGCAGGCCCCGCGGTCCAGGGATGGCGGGGCTAGTAGTACCGGCAGCC  
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGC  
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGG  
CCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCA  
TGGATAGCAGCGCCGCCTTCCTGCAGGGGCTGTGGCAGCACTACCACCTGGCTTGCCGCCGC  
CGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTG  
ATCATGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTTATCACGTGGAAG  
CCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC  
CAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTCACCTGTTCAATTTGACCTGG  
CAATTAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAG  
AATATTTAAATCTGAAACAATATTGGAAGAGGATATGGGTATACTATTAACAGTCGAT  
CCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGCAGTTGAACAGAAACAA  
GGTCTCAGCCAATTTCTTCTCCAGTCATCTCCAGTTTGGTCATGCAGAGACTCTTCTTCCAC  
TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAC  
AAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGTGC  
TTTACCCTGTGAAATGCTAAGACTCCTAAAGAACAATTCCGAGTGCAGATGTTATTAAATG  
AAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACC  
ACTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGAATGTGAATTAGCAAGGGCTAACA  
GTACATCTGATGAAC**TGAG**TAACTGAAGAACATTTTTAATTCTTTAGGAATCTGCAATGAG  
TGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAG  
TATTTCTGTCTTTTACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGA  
AAAGATTTTTCAGTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGC  
CCTGCAAATGTTTACAGAAATGAAATCTTCTACTTATATAAGAAATCTCACACTGAGATAG  
AATTGTGATTTTATAATAACACTTGAAAAGTGCTGGAGTAACAAAATATCTCAGTTGGACCAT  
CCTTAACTTGATTGAAC**TGAG**TAAGTCTAGGAACCTTACAGATTGTTCTGCAGTTCTCTCTTTTCC  
TCAGGTAGGACAGCTCTAGCATTTTCTTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACT  
CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTGTAAAAGGAC  
ACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAATATTTTTGGTATTTATTTATGAA  
ATATTTGAACATTTTTTCAATAATTCCTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAA  
ATTATTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCC  
ATTGCTTAGCTAACTTTTTTCAATTCTGTCACTTGGCTTCGATTTTTATATTTTCTATTATATG  
AAATGTATCTTTTGGTTGTTTGATTTTTCTTTCTTTGTAATAGTTCTGAGTTCTGTCA  
AATGCCGTGAAAGTATTTGCTATAATAAGAAAATTCCTGTGACTTTAAAAA

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**FIGURE 528**

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLSG  
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRLHGLLQARGSRDGGASSTGSRD  
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD  
SSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF  
KTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEDLAIKGVKSPWCDVFDIDDAKVLEY  
LNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL  
SLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK  
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

**Important features:****Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

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**FIGURE 529**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGG  
CGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA  
CGCGGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG  
GTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGGGCTC  
TTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAAATGGT  
ACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC  
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTCCCAAGGG  
CAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAGACCTTGAC  
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT  
GATGTCAAAAACCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCTGTAGAA  
AAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCTTA  
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAAACTCTAAACGG  
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGCTCCTCGGAAGTCC  
CCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACCAGGGCCAGTCATA  
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG  
GTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA  
ACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTAACCATGTAGCCTTGGAGACCCAGG  
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA  
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTCATGATGAAAAGATGGTATGATTC  
TACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTCAGGTCATTTACAATTGGGAG  
ATTTTCAGAAACATTCCCTTTCACCATCATTTAGAAATGGTTTGCCTTAATGGAGACAATAGCAG  
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA  
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC  
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTG  
AAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACTAAAATATGGGGCAATTGTTAGCCTT  
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTGAAATGTGTATATCAATTTCTGGATT  
CATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCATTTCATTCTGGACACAGTTGGAT  
CAATACTGATTAAGTAGAAAATCCAAGCTTTGCTTGAGAACTTTTGTAACGTGGAGAGTAAAA  
AGTATCGGTTTTTA

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**FIGURE 530**

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST  
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIENMQ  
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMILAV  
LYRRKNSKRDTGCTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS  
DKINKSESVYADIRKN

**Important features:****Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

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**FIGURE 531**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA  
GGCTGGTGGGAAGAAGCCGAG**ATG**GGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC  
TTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACTGGT  
GCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCCTGTGGCACGGTGGGGCTGCTGCTG.  
GAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCTGGAAC  
CAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC  
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGGGGCCCTG  
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG  
CACCTGTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTCGGTG  
GTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC  
ACCTCGGTGCAGCTGCAGCCGCCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG  
CGCCTGGAGATGGAACAGGCCCAAGAAGGCCAAGAACCCCCAGGAGCAGAAGTCCTTCTTCGCC  
AAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAGGAGCGCCAGACACC  
GGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCA  
CCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTTGAAAA  
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCTGATGTACAAGCT  
TGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAGGAATGGCTGTCCCCATC  
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCCAGATC  
GACACGCAAAAAAAAAA

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**FIGURE 532**

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID  
DSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEAGG  
YVSSFVPACSLVESHLS DQLTLHVDVAGNVVGVS VVTHPGGCRGHEVEDVDLELFNTSVQLQP  
PTTAPGPETA AFIERLEMEQAQKAKNPQE QKSFFAKYW MYIIPVVLFLMMSGAPDTGGQGGGG  
GGGGGGGSGLCCVPPSL

**Important features:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243



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## **FIGURE 534**

MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWC  
CQTHDCCYDHLKTQGCGLYKDNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70



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**FIGURE 535**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG  
AACTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC  
CCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT  
TTTTTAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCAT  
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTTGCTGCGAATGCGGTGTTGGGATTTATTT  
GTTCTTGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG  
GGTCCAATTTTTCTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG  
CTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAA  
AGGATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCC  
ACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA  
GGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGT  
TGCTTAGGTTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGG  
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT  
TTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAATCTCCTATTTTTCTT  
AACAATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCTTATAATCAGCTGCAT  
TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTTACATTTACGGTCTAAC  
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAACCTTTTGGACCTG  
GGATATAACCGGATCCGAAGTTTAGCCGAAGATGTCTTTGCTGGCATGATCAGACTCAAAGAA  
CTTACCTGGGACACAATCAATTTTCCAAGCTCAACCTGGCCCTTTTTCCAAGGTTGGTCAGC  
CTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGTGCATAGGACAGACCATGTCCTGGACC  
TGGAGACTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT  
GTTTTCCAGTGTGTCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT  
GGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG  
GAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG  
AATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG  
AACTACAGCATCTGTGGCAAAGTACTACAGAGAGGTTTTGATCTGGCCAGGGCTCTCCCAAAG  
CCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTTTGCCCCGACG  
GTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCTTTCCATAAA  
ATCATCGCGGGCAGCGTGGCGCTTTTCCTGTCCGTGCTCGTCATCCTGCTGGTTATCTACGTG  
TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC  
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTAGAT  
TATAAACCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTAT  
AACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAAGC  
TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC  
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCCGTTTTAGTGCATTCATA  
ATACTGGTCATTTTCCCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGT  
GAAGCTTGAACCTCCGGTTTAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAAT  
GTCGCATTTGTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

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**FIGURE 536**

MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC  
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELIILSSNRISYFLN  
NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELLDLG  
YNRIRSLARNVFAGMIRLKELHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTMSWTW  
SSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDSENKLTFIGQEILDSWISLNDISLAGNIWE  
CSRNICSLVNWLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLARALPKP  
TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVS  
WKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCCTYN  
KSGSRECEV

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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**FIGURE 537**

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGC  
AGACAAGTGACCCCAAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAA  
TTCAGGGGAGACTTGGCGGGTCTGTCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTGCTTGTCTGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGGCGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCCACGGATT  
CCAGAGCCAATCCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCGAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCCTTGTCTGACTGGCCCTGA  
TCAGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACAGATGGAGTTAACTACATCCGCACCTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAGCCACATGAATAGAAGATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGTCTACGTAACGCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCAACACTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTGTTGTAACCAACCAAAATCAGGAAG  
GTAAATTTGGTTGCTGGAAGAGGGATCTTGCCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTGTTTATTTTATAAAATTT  
TACATCTAAATTTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT  
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT  
CACACAAGTTTTAGCCTTTTTTACAAGGGAACCTCATCTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAGTTTGTTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCCTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTTATCCGCGGAGACACTGCTCCCAT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTTCAAGTGTCTTGGGTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTGTTTAAAC  
CTCATTTATAAAAGCTTCAAAAAACCCA

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**FIGURE 538**

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS DP  
RIEWKKIQDEQTTYVFFDNKIQQDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVARNDRKEI  
DEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPR  
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDYDLNIGGIIGGVLVV  
LAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features:****Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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**FIGURE 539**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAGC  
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCTCTAGGACATACACGGGACCCCTAA  
CTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGG  
CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGG  
GCTCGGGCGGCGGGAGTAGGGCCCCGGCAGGGAGGCTGCATATTCAGAGTTCGCGGG  
CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGA  
**TG**AGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC  
GCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG  
CCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCTGGCTTGTGAGAGTG  
AGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC  
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGA  
ATGGAGATGGGCAAACATCTGGTGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT  
CCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGT  
ATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCAGTGGAATGATGACA  
GGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCCTG  
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG  
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACCCCTGCTCTTACTGATAC  
TGTTTGCTTTTGGAACCTGTTGTTTCCAGATGCTGCATAAAAAGTAAAGGAAGAACAAAACCTA  
GTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAGTAT  
**AA**TAACTCATTGACTTGGTTCCAGAATTTTGTAATTTCTGGATCTGTATAAGGAATGGCATCAG  
AACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAAGATGAACTGTAAGCTCCCCCT  
TGAGGCCAAATATTAAAGTAATTTTTATATGTCTATTATTTTCAATTTAAAGAATATGCTGTGCTA  
ATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAAACTTCAAACCTTCAAGCAAA  
TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT  
TCCTTTTATTTCTTTTACCTTTTACATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA  
AATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAAATGAACTGTTCTA  
ATATTTATTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAGAACTTATTAC  
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGTTTTCTCGAA  
ATAATTCATCTTTTACGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA  
AGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT  
AATTTCAATTGTGCAAGACATGTGCCTTATAATTTATTTTATAGCTTAAATTTAAACAGATTTTG  
TAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAGT  
GACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTG  
AGGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTT  
GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC  
CTCTGACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAG  
TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAGGAAGTACGAAATCGTGTGAAA  
ATGGGTTGGAACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATG  
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGA  
AAGTTGTAACCTCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAATAAAGAGTTCTTG  
TTTCTGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 540**

MSRVVSLLLGAALLCGHGAFRCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACES  
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGFWIGLWRNGDGQTSACPDLYQWSDGSN  
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP  
VEKPYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKT  
SPNQSTLWISKSTRKESGMEV

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89 and 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

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**FIGURE 541**

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
CCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCTGGGTGCTGTGCGAGGCCGGCAGGTGG  
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCCGAGC  
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCAATGTGCCTAC  
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
GCCTGGTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG  
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTG  
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC  
ACAGAGCCATCACACAGAGTGGGGTCATCACCACCCCAGGGATCATCGACTCTCACCCTTGGCCCCCTAGCTCAGA  
AAATCGCAAACACCTTGGCCTGCAGTCCAGTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
GCTGGCTCATCCCCAGGGGCTGGGGTCTCTGGATAACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
CAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA  
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCAGGAATTCATGGGTGACGTATTTCATCAATGTTCCACCGTCA  
GTTTTCAAGATACTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG  
CGAAGATCAAACCTGCCTGGGTGAAGCTGATCATGGGGCCGAGGGTGCTTTTGTGTTGCGAGGTCCCTTCCTCA  
TGGACGAGAGCTCCCGCTGGCCTTTCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCACCAGGCGG  
AACATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG  
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCCAGGAGGACCTCTGAGGCC  
AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCAGCACGGCAGCCCGCCTCTC  
CCCCGTCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
ATGTCACAAGGCCGCTCCACCTCTGGGGCATTGTACAAGTCTTCCCTCTCCCTGAAGTGCCTTTCCTGCTTT  
CTTCGTGGTAGGTTCTAGCACATTCTCTAGCTTCCCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC  
TGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT  
CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTCACCCACACCAGGATCGGGTGGGA  
CCTGGAGCTAGGGGGTGTGCTGAGTGAGTGAGTGAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC  
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC  
AATGGCAGAGACCTGGGATGGGAGAAGTCTTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCGAC  
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTGGCCCCCTGCACAAGACAACAGA  
ATCCATCAGGGCCATGAGTGTCACCAGACCTGACCCTCACCAATTCCAGCCCCCTGACCCTCAGGACGCTGGATG  
CCAGTCCCAGCCCCAGTGCCGGTCTCCTCCTTCTTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG  
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGCGGCTATTGTACA  
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGGTTTTTCAGATGGAAGTGAGAG  
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCCTGCCGCTCTGCCTGGGCTCCCACTTTGGCA  
GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAAGCCGGAGCCAGCT  
CCCTCAGCTTGGCGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGGGCCAG  
AGTGAGTTCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGCGCT  
TAGCACCTGGGCCAGCAGCTGTGTGCTCGATTTCTCGTGGGCCTTAGCTGCCTCCCCGCGGGGCGAGGCTCGG  
GACCTGCAGCCCTCCATGCCTGACCCTCCCCCACCCTCGTGGGCTCCTGTGCGGCGGAGCCTCCCCAAGGAG  
CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGAGTGGGGTGACAGCGCGGGA  
CTGGCAGGCAGCTCCACCTGCTGCCCACTGCTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG  
GACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT  
TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
ACTCTGGTGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCTGTCAAACAGACCACTTGACTCTCTGTAAAT  
GGACCAATCAGCAGGATGTGGGTGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
CCCTCGGGTCCCCTCCCACGCCGTGGAAGCTTTGTTCTTTCGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

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**FIGURE 542**

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGVKGTDRLVNVFLGI  
PFAQPPLGPD RFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV  
LNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAYGDVVVVTVQYRLGVLGFFSTG  
DEHAPGNQGF LDDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIIISGLVLS PVAAGLFHRAI  
TQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT  
VDGTVFPKSPKELLKEKPFHSPFLMGVNNHEFSWLI PRGWGLLD TMEQMSREDMLAISTPVL  
TSLDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF  
QHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMM AQWTHFA  
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA  
QEDL

**Important features:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 226-245

**N-glycosylation site.**

amino acids 105-109

**N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**Carboxylesterases type-B serine active site.**

amino acids 216-232



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**FIGURE 543**

TGTCGCCTGGCCCTCGCCATGCAGACCCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA  
CTGGGGGGCGCCACGGCCTCTTTCCTGAGGAGCCGCCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTTTGTGGGCAGCGGGCCCCGACGCCTGACCCCCGAGAAGGTGCTGACGACCTCAACATCCAGCGA  
GTCCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCACGCGACATAAACGTGTGTGGATGAAG  
GGCAAACAGGAGGGCGAGTGTGCGAACTTCGTAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTTCCAACGCCCTCAACCCGGTGTGCGCCAACCTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC  
GGTATGGCCCGCTGCCCCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTACAGCT  
ACTGTTACCGACTTCCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCCCACCCTGCGCACCCTG  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
TTCCGGGAGATTGCGATGGAGTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCTGGCCCCGAGTGTGCAAGAAC  
GACGTGGGAGGCTCCCCCGCGTGCTGGAGAAGCAGTGGACGTCCTTCTGAAGCGCGGCTCAACTGCTCTGTA  
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCGGCCCGTG  
GTCCTGGCCGTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG  
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAG  
GTGCCTCGACCCCGCCCGGGTGCTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC  
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG  
CGGACCCTGATGAGGCACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCTGGGGCAACAGACCGTT  
GTCTTCTGGGTCTGAGGCGGGGACGGTCCTCAAGTTCTCGTCCGGCCCAATGCCAGCAGCTCAGGGACGTCT  
GGGCTCAGTGTCTTCTGGAGGAGTTTGAACCTACCGGCCGACAGGTGTGGACGGCCCCGGCGGTGGCGAGACA  
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCCGGGGGCGCTGCTGGCTGCCCTTCCCCCGCTGCGTGGT  
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC  
GGGTGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCTTTGAGCAGGACGTGTCCGGG  
GCCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG  
TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCCTCGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC  
TGGTTCTGTTGGCCTCCGTGAGCGGCGGGAGCTGGCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG  
GGCGAGGCGGTGTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGCGGAGGCGGT  
GGCGGTGGCGCCGGGTTCCCCCGGAGGCCCTGCTGGCGCCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
CTGACGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCCCAGCCGAGCAGACGCGCTGCCGAGAAGCGC  
CTGCCACTCCGCAACCCGACCCCCACGCCCTGGGCCCCCGCGCCTGGGACCCAGCCAGGCCACCCCCCTGCTCCCGGCC  
TCCGCTTATCTCTCCCTCCTGCTGCTGGCGCCCCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC  
CCCGACGGCCGCTCTATGCTGCCCGGGCCGCGCGCCTCCACGGCGACTTCCCGCTCACCCCCACGCCAGC  
CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCCCTTGGACCCAGCCTCAGCCGCCGATGGCCTCCCGCGG  
CCCTGGAGCCCGCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCTGCGC  
CGCACCCACAGTTCAACAGCGGCGAGGCCCGGCTGGGGACCGCCACCGCGGCTGCCACGCCCGGCCGGGACA  
GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGCCCTTAGCGCGGGGGCCCCCG  
ATGCCTTGGCAGTGCCAGCCACGGGAACAGGAGCGAGAGCGGTGCCAGAACGCCGGGGCCCCGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCGCGACCCACCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAACCAG  
CTCGCCCTCCCCCTACCCGGGGCCGACGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG  
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTGAGTTTTGGTTTTCTTTGCGGTTTTCTAACC  
AATTGCACAACTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGGACGCCGCTGGGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG  
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCCGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG  
TGGGCGTGTGTGTAAGTGGGCCACGCGTGCAGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGGTATAGGATTTGAAC  
CCCCCCTCTCTGAGAGGGAAGCGGGGACAATGCCGGGTTTTCAGGCAGGAGACAGGAGGCGGCTGGGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA  
ATACGGCCCCAGGTGGTGAGAGAGTCCATGCCACCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCTCCCCCAGCCCCCTCCCCATCAAT  
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 544**

MQTPRASPPRPALLLLLLLLGGAGHLFPEEPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGAD  
DLNIQRLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC  
RNFVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG  
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFREIAMEF  
NYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG VVSLG  
GRP VVLAVFSTPSNSIPGSAVCAFDLTQVA AVFEGRFREQKSPESI WTPVPEDQVPRPRPGCC  
AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTL MRHQLTRVAVDVGAGPWGN  
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQRLLSLELD  
AASGGLLA AFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTRAAFEQDV  
SGASTSGLGDC TGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGWFVGLRERREL  
ARRKDKEAILAHGAGEAVLSVSR LGERRAQGPGGGGGGGGAGVPPEALLAPLMQNGWAKAT  
LLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLPASASSLLLLAPA  
RAPEQPPAPGEPTPDGRLYAARPGRASHGDFLTPHASPDRRRVVSAPTGPLDPASAADGLPR  
WSPFPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHL LPYGGADR  
TAPPVP

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 318-339, 598-617

**N-glycosylation sites.**amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation sites.**amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885

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**FIGURE 545**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTTCACTGCAAGTGCCTGCTGTT  
CCAGGCCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCCTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCGATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAATAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATTAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 546**

MRQFPKTSFDISPMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPE  
IFSSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE  
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY  
TLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAADVVKALGELDI  
LLQWMEETE

**Important features:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

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**FIGURE 547**

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGCA  
GAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTTCGCG  
GAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA  
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTCATTT  
ATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATTGCTTC  
TTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCGGAGAAG  
AGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTTCTATATT  
CAGGCAGTGGATACATCAGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG  
AAAGTCTCAGCACCAGAGGAGCAATTCCTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT  
GGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAATCTGAAGGTGGAAATTAA  
TTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAAGGGCCGGTTTACCATGAGAAC  
TGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT  
GCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA  
ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAAAGGATAACAAGGTT  
TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGATGCCATACTACTTTCT  
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTTGGGAGACTGGCCTTTG  
GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGTGTGGCTCCACAGATTCC  
AAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATGGGCCGGGTA  
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTGGGAAAGCAAAAATTCCTACT  
GCCGTCTGGAGAGGGCGAGACAGCCGAAAGAGAGACTCGAGCTGGTTAAACTCAGTAGAAAA  
CACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTCTTTAAACACGATGAAAACCTG  
TATGGTCCCATTGTGAAACATATTTCAATTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT  
ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTTGTGCTG  
AAGCAGGATTCATCTACTATGAACATTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT  
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACTTAAATGGGCGAAAGATCACGATGAA  
GAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC  
ATATTCTGTTATTATTTCAAACCTTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA  
ATCCGAGAGGGCATGAAAAGGGTAGAACCACAGACTGAGGACGACCTCTTCCCTTGCTACTTGC  
CATAGGAAAAAGACCAAGATGAACTCTGATATGCAAAATAACTTCTATTAGAATAATGGTGC  
TCTGAAGACTCTTCTTAACTAAAAAGAAGATTTTTTTAAGTATTAATTCCATGGACAATATA  
AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG  
TACTTTAAAGTACATTTTTAGAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAAA

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**FIGURE 548**

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLARYFYIQA VDTSGNKFT  
SSPGEKVFQVKVSAPEEQFTRVGVQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKSPY  
ILKGPVYHENCDCPLQDSA AAWLREMNC PETIAQIQRD LAHFPAVDPEKIAVEIPKRFGQRQSL  
CHYTLKDNKVYIKTHGEHVGFRI FMDAILLSLTRKVKMPDVELFVN LGDWPLEKKKSNSNIHP  
IFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGRDSRKE  
RLELVKLSRKHP ELIDAAFTNFFFFKH DENLYGP IVKHISFFDFFKH KYQINIDGTVAAYRLP  
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKS NLSDLLEKLKWAKDHDEEAKKIAKAGQE  
FARNNLMGDDIFCY YFKLFQ EYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 302-306, 414-418

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

**Tyrosine kinase phosphorylation site.**

amino acids 341-348

**N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

**Endoplasmic reticulum targeting sequence.**

amino acids 499-504

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**FIGURE 549**

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTGC  
CTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGG  
GTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC  
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA  
AGGACTCACCTCCCAAAAATTCCGTGAAGGTTGATGAGCTTTCACTCTACTCAGTTCCTGAGG  
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC  
ACTATTGCGAGCCATACACAACCTGGTGTCAGGAAACGTA CTCCCAAATAAGCCCAAGATGC  
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT  
TTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA  
AAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC  
AACAAGCCATCGTGTTTGCCCAGGTCAGTGGGGAGAGATTATATGACTGGGGTTTACGAGGAT  
ATATAGTCATAGAAGATTTGTGGAAGGAGAACTTTCAAAGCCAGGAAATGTGAAGAATTCAC  
CTGGAATAAGTAGAAAACCTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA  
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA  
AATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCT  
ACAAGCAAATAACCTGGAATCCCTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT  
TCTCATGTTGCTATTTATGTACCTAATTAAACCCAAGTTTAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

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## **FIGURE 550**

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES  
ISQLRHYPEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL  
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG  
NVKNSPGTK

**Important features:**

**Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 111-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 36-44

**N-myristoylation sites:**

Amino acids 124-130;144-150;189-195



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International Bureau(43) International Publication Date  
7 June 2001 (07.06.2001)

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(10) International Publication Number  
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		PCT/US99/30999	20 December 1999 (20.12.1999)	US
(21) International Application Number:	PCT/US00/32678	PCT/US99/31243	30 December 1999 (30.12.1999)	US
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(30) Priority Data:		PCT/US00/03565	11 February 2000 (11.02.2000)	US
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PCT/US99/28564	2 December 1999 (02.12.1999)	PCT/US00/04914	24 February 2000 (24.02.2000)	US
PCT/US99/28565	2 December 1999 (02.12.1999)	PCT/US00/05004	24 February 2000 (24.02.2000)	US
60/170,262	9 December 1999 (09.12.1999)	PCT/US00/05601	1 March 2000 (01.03.2000)	US
PCT/US99/30095	16 December 1999 (16.12.1999)	PCT/US00/05841	2 March 2000 (02.03.2000)	US

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGR  
 QQQKKIERQEEKLKNNNRDLSMVRMKSMAIGFCFTALMGMFNSIFDGRVAKLPFTPLSYIQ  
 GLSHRNLLGDDTTDCSFI FLYILCTMSIRQNIQILGLAPSRAATKQAGGFLGPPPPSGKFS

**Important features:****Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

WO 01/40466 A3



- |                |                                |    |  |
|----------------|--------------------------------|----|--|
| 60/187,202     | 3 March 2000 (03.03.2000)      | US | (US). <b>SHERWOOD, Steven</b> [US/US]: 995 Lundy Lane, Los Altos, CA 94024 (US). <b>SMITH, Victoria</b> [AU/US]: 19 Dwight Road, Burlingame, CA 94010 (US). <b>STEWART, Timothy, A.</b> [US/US]: 465 Douglass Street, San Francisco, CA 94114 (US). <b>TUMAS, Daniel</b> [US/US]: 3 Rae Avenue, Orinda, CA 94563 (US). <b>WATANABE, Colin, K.</b> [US/US]: 128 Corliss Drive, Moraga, CA 94556 (US). <b>WOOD, William, I.</b> [US/US]: 35 Southdown Court, Hillsborough, CA 94010 (US). <b>ZHANG, Zemin</b> [CN/US]: 876 Taurus Drive, Foster City, CA 94404 (US). |
| PCT/US00/06319 | 10 March 2000 (10.03.2000)     | US |  |
| PCT/US00/06884 | 15 March 2000 (15.03.2000)     | US |  |
| PCT/US00/07377 | 20 March 2000 (20.03.2000)     | US |  |
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| PCT/US00/14941 | 30 May 2000 (30.05.2000)       | US |  |
| PCT/US00/15264 | 2 June 2000 (02.06.2000)       | US |  |
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| PCT/US00/23522 | 23 August 2000 (23.08.2000)    | US |  |
| PCT/US00/23328 | 24 August 2000 (24.08.2000)    | US |  |
| 60/000,000     | 15 September 2000 (15.09.2000) | US |  |
| PCT/US00/30952 | 8 November 2000 (08.11.2000)   | US |  |
| PCT/US00/30873 | 10 November 2000 (10.11.2000)  | US |  |
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- (72) **Inventors; and**
- (75) **Inventors/Applicants (for US only): BAKER, Kevin, P.** [GB/US]; 14006 Indian Run Drive, Darnestown, MD 20878 (US). **BERESINI, Maureen** [US/US]; 611 Stetson Street, Moss Beach, CA 94038 (US). **DEFORGE, Laura** [US/US]; 1175 Manzanita Drive, Pacifica, CA 94044 (US). **DESNOYERS, Luc** [CA/US]; 2050 Stockton Street, San Francisco, CA 94133 (US). **FILVAROFF, Ellen** [US/US]; 538 18th Avenue, San Francisco, CA 94121 (US). **GAO, Wei-Qiang** [CN/US]; 641 Pilgrim Drive, Foster City, CA 94404 (US). **GERRITSEN, Mary, E.** [CA/US]; 541 Parrott Drive, San Mateo, CA 94402 (US). **GODDARD, Audrey** [CA/US]; 110 Congo Street, San Francisco, CA 94131 (US). **GODOWSKI, Paul, J.** [US/US]; 2627 Easton Drive, Burlingame, CA 94010 (US). **GURNEY, Austin, L.** [US/US]; 1 Debbie Lane, Belmont, CA 94002 (US). **SHERWOOD, Steven** [US/US]; 995 Lundy Lane, Los Altos, CA 94024 (US). **SMITH, Victoria** [AU/US]; 19 Dwight Road, Burlingame, CA 94010 (US). **STEWART, Timothy, A.** [US/US]; 465 Douglass Street, San Francisco, CA 94114 (US). **TUMAS, Daniel** [US/US]; 3 Rae Avenue, Orinda, CA 94563 (US). **WATANABE, Colin, K.** [US/US]; 128 Corliss Drive, Moraga, CA 94556 (US). **WOOD, William, I.** [US/US]; 35 Southdown Court, Hillsborough, CA 94010 (US). **ZHANG, Zemin** [CN/US]; 876 Taurus Drive, Foster City, CA 94404 (US).
- (74) **Agents: KRESNAK, Mark, T. et al.:** Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).
- (81) **Designated States (national):** AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:**  
— with international search report
- (88) **Date of publication of the international search report:**  
10 May 2002
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/32678

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47 C07K14/705 C12N15/62 C07K16/18  
 C07K16/28 G01N33/53 A61K38/17 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K G01N A61K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 21328 A (KATO SEISHI ;PROTEGENE INC (JP); SEKINE SHINGO (JP); SAGAMI CHEM R) 22 May 1998 (1998-05-22) * see seq.ID's.12, 37 and 62: clone HP10122 *	1-20, 69-71
X	WO 99 09061 A (GENETICS INST) 25 February 1999 (1999-02-25) * see clone am910_li * --- -/--	1-20

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&amp;" document member of the same patent family

Date of the actual completion of the international search

8 August 2001

Date of mailing of the international search report

12.11.01

Name and mailing address of the ISA

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/32678

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	IWAMURO SHAWICHI ET AL: "Multi-ubiquitination of a nascent membrane protein produced in a rabbit reticulocyte lysate." JOURNAL OF BIOCHEMISTRY (TOKYO), vol. 126, no. 1, July 1999 (1999-07), pages 48-53, XP002174228 ISSN: 0021-924X the whole document ---	1-20
X	DATABASE EMBL [Online] Entry/Acc.no. AF070626, 2 July 1998 (1998-07-02) ANDERSON, B ET AL.: "Homo sapiens clone 24483 unknown mRNA, parital cds." XP002174229 the whole document ---	1-20
A	EP 0 834 563 A (SMITHKLINE BEECHAM CORP) 8 April 1998 (1998-04-08) the whole document ---	
A	WO 97 07198 A (GENETICS INST) 27 February 1997 (1997-02-27) the whole document ---	
A	KLEIN R D ET AL: "Selection for genes encoding secreted proteins and receptors" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA,US,NATIONAL ACADEMY OF SCIENCE. WASHINGTON, no. 93, 1 July 1996 (1996-07-01), pages 7108-7113, XP002077277 ISSN: 0027-8424 the whole document ---	
A	YOKOYAMA-KOBAYASHI M ET AL: "A signal sequence detection system using secreted protease activity as an indicator" GENE,NL,ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, vol. 163, no. 2, 3 October 1995 (1995-10-03), pages 193-196, XP004041983 ISSN: 0378-1119 the whole document ---	
P,X	WO 00 37630 A (GENETICS INST) 29 June 2000 (2000-06-29) * see clone AM910_li * -----	1-13, 17-20

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 00/32678

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 and 69-71, all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-20 and 69-71, all partially

PRO177: nucleic acid with seq.ID.1, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.2 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.2 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide.

Inventions 2-242: claims 1-20 and 69-71,  
all partially

Subject matter as defined for invention 1, but related to the respective nucleic acid/polypeptide sequences of:

Invention 2: PRO3574, represented by seq.ID.s 3 and 4,

Invention 3: PRO1280, represented by seq.ID.s 5 and 6,

Invention 4: PRO4984, represented by seq.ID's 7 and 8,

...

Invention 15: PRO1471, represented by seq.ID.s 29 and 30,  
(PRO1114 skipped; follows below)

Invention 16: PRO1076, represented by seq.ID.s 33 and 34, ...

Invention 92: PRO4345, represented by seq.ID.s 185 and 186,  
(PRO4978 skipped; follows below)

Invention 93: PRO4327, represented by seq.ID.s 221 and 222,

...

Invention 107: PRO6028, represented by seq.ID.s 217 and 218,  
(PRO100 skipped; follows below)

Invention 108: PRO4327, represented by seq.ID.s 221 and 222,

...

Invention 132: PRO197, represented by seq.ID.s 269 and 270,  
(PRO195 skipped; follows below)

Invention 133: PRO187, represented by seq.ID.s 273 and 274,  
(PRO182 skipped; follows below)

Invention 134: PRO188, represented by seq.ID.s 277 and 278,

...

Invention 136: PRO184, represented by seq.ID.s 281 and 282,  
(PRO185 skipped; follows below)

Invention 137: PRO200, represented by seq.ID.s 285 and 286,  
(PRO202 skipped; follows below)

Invention 138: PRO214, represented by seq.ID.s 289 and 290,  
(PRO215 skipped; follows below)

Invention 139: PRO219, represented by seq.ID.s 293 and 294,  
(PRO211 skipped; follows below)

Invention 140: PRO220, represented by seq.ID.s 297 and 298,  
(PRO366, PRO216, PRO221 skipped; follows below)

Invention 141: PRO228, represented by seq.ID.s 305 and 306,

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

(PRO217, PRO222, PRO224 skipped: follows below)  
 Invention 142: PRO230, represented by seq.ID.s 313 and 314,  
 (PRO198 skipped: follows below)  
 Invention 143: PRO226, represented by seq.ID.s 317 and 318,  
 ...  
 Invention 151: PRO323, represented by seq.ID.s 333 and 334,  
 (PRO245 skipped: follows below)  
 Invention 152: PRO246, represented by seq.ID.s 337 and 338,  
 ...  
 Invention 155: PRO257, represented by seq.ID.s 343 and 344,  
 (PRO172 skipped: follows below)  
 Invention 156: PRO258, represented by seq.ID.s 347 and 348,  
 (PRO265 skipped: follows below)  
 Invention 157: PRO326, represented by seq.ID.s 351 and 352,  
 (PRO266 skipped: follows below)  
 Invention 158: PRO269, represented by seq.ID.s 355 and 356,  
 ...  
  
 Invention 160: PRO328, represented by seq.ID.s 359 and 360,  
 (PRO344 skipped: follows below)  
 Invention 161: PRO272, represented by seq.ID.s 363 and 364,  
 (PRO301 skipped: follows below)  
 Invention 162: PRO331, represented by seq.ID.s 367 and 368,  
 ...  
 Invention 165: PRO310, represented by seq.ID.s 373 and 374,  
 (PRO337 skipped: follows below)  
 Invention 166: PRO346, represented by seq.ID.s 377 and 378,  
 Invention 167: PRO350, represented by seq.ID.s 379 and 380,  
 (PRO526 skipped: follows below)  
 Invention 168: PRO381, represented by seq.ID.s 383 and 384,  
 ...  
 Invention 173: PRO731, represented by seq.ID.s 393 and 394,  
 (PRO322 skipped: follows below)  
 Invention 174: PRO536, represented by seq.ID.s 397 and 398,  
 (PRO719 skipped: follows below)  
 Invention 175: PRO619, represented by seq.ID.s 401 and 402,  
 ...  
 Invention 214: PRO1475, represented by seq.ID.s 479 and 480,  
 (PRO1312 skipped: follows below)  
 Invention 215: PRO1308, represented by seq.ID.s 483 and 484,  
 ...  
 Invention 222: PRO1358, represented by seq.ID.s 497 and 498,  
 (PRO1286 skipped: follows below)  
 Invention 223: PRO1294, represented by seq.ID.s 501 and 502,  
 Invention 224: PRO1273, represented by seq.ID.s 503 and 504,  
 (PRO1279 skipped: follows below)  
 Invention 225: PRO1195, represented by seq.ID.s 507 and 508,  
 Invention 226: PRO1271, represented by seq.ID.s 509 and 510,  
 (PRO1338, PRO1343 skipped: follows below)  
 Invention 227: PRO1434, represented by seq.ID.s 513 and 514,  
 ...  
 Invention 237: PRO1693, represented by seq.ID.s 536 and 537,

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(PR01868 skipped: follows below)

Invention 238: PR01890, represented by seq.ID.s 539 and 540,

...

Invention 240: PR04353, represented by seq.ID.s 543 and 544,  
(PR01801 skipped: follows below)

Invention 241: PR04357, represented by seq.ID.s 547 and 548,

Invention 242: PR04302, represented by seq.ID.s 549 and 550.

For the sake of conciseness, the first subject matter is explicitly defined, the subject matter of inventions 2-241 are defined by analogy thereto, whereby the numbering of the sequences is followed, except for sequences which are mentioned in one of claims 21-68; inventions relating thereto follow below.

Invention 243: claims 43-49, 53, 54 completely,  
and claims 1-24, 29-31, 35, 36, 69-71,  
all partially

PR01114: nucleic acid with seq.ID.31, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.32 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.32 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR01801 and/or PR0100 using their interactions with PR01114, method for linking a bioactive molecule to a cell expressing PR01801 and/or PR0100 through the use of PR01114, and method of modulating at least one activity of said cell thereby.

Invention 244: claims 1-24, 29-31, 35, 36, 53, 54,  
69-71, all partially

PR04978: nucleic acid with seq.ID.187, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.188 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.188 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR01801 using its interaction with PR04978, method for linking a bioactive molecule to a cell expressing PR01801 through the use of



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PR04978, and method of modulating at least one activity of said cell thereby.

Invention 245: claims 39-42, 50-52, 55,  
56 completely, and claims 1-20, 69-71,  
all partially

PR0100: nucleic acid with seq.ID.219, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.220 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.220 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR01801 and/or PR01114 using their interactions with PR0100, method for linking a bioactive molecule to a cell expressing PR01801 and/or PR01114 through the use of PR0100, and method of modulating at least one activity of said cell thereby.

Invention 246: claims 1-20, 57, 69-71,  
all partially

PR0195: nucleic acid with seq.ID.271, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.272 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.272 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR0195 protein.

Invention 247: claim 66 completely,  
and claims 1-20, 58, 59, 69-71, all partially

PR0182: nucleic acid with seq.ID.275, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.276 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.276 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of

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said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for inhibiting the binding of A-peptide to factor VIIA using the PRO182 protein.

Invention 248: claims 1-20, 67, 69-71,  
all partially

PRO185: nucleic acid with seq.ID.283, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.284 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.284 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for inhibiting the differentiation of adipocytes using the PRO185 protein.

Invention 249: claims 1-20, 57, 59, 60, 69-71,  
all partially

PRO202: nucleic acid with seq.ID.287, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.288 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.288 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for stimulating the proliferation or differentiation of chondrocytes, and method for modulating the uptake of glucose or FFA by adipocytes using the PRO202 protein.

Invention 250: claims 1-20, 57, 69-71,  
all partially

PRO215: nucleic acid with seq.ID.291, encoding a polypeptide comprising the amino acid sequence as represented in

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seq.ID.292 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.292 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR0215 protein.

Invention 251: claims 1-20, 60, 69-71,  
all partially

PR0211: nucleic acid with seq.ID.295, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.296 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.296 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by adipocytes using the PR0211 protein.

Invention 252: claim 61 completely,  
and claims 1-20, 58, 59, 69-71, all partially

PR0366: nucleic acid with seq.ID.299, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.300 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.300 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for stimulating the proliferation of gene expression in pericytes using the PR0366 protein.

Invention 253: claim 62 completely,  
and claims 1-20, 69-71, all partially

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PRO216: nucleic acid with seq.ID.301, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.302 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.302 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of proteoglycans from cartilage using the PRO216 protein.

Invention 254: claims 1-20, 57, 69-71,  
all partially

PRO221: nucleic acid with seq.ID.303, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.304 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.304 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO221 protein.

Invention 255: claims 1-20, 69-71, all partially

PRO217: nucleic acid with seq.ID.307, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.308 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.308 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO217 protein.

Invention 256: claim 68 completely,  
and claims 1-20, 69-71, all partially

PRO222: nucleic acid with seq.ID.309, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.310 or a nucleic acid having at least 80% homology

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thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.310 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, and method for stimulating the proliferation of endothelial cells using the PR0222 protein.

Invention 257: claims 1-20, 59, 69-71,  
all partially

PR0224: nucleic acid with seq.ID.311, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.312 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.312 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, and method for stimulating the proliferation or differentiation of chondrocytes using the PR0224 protein.

Invention 258: claims 1-20, 57-59, 67, 69-71,  
all partially

PR0198: nucleic acid with seq.ID.315, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.316 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.316 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for inhibiting the differentiation of adipocytes using the PR0198 protein.

Invention 259: claims 1-20, 57, 69-71,

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all partially

PR0245: nucleic acid with seq.ID.335, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.336 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.336 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR0245 protein.

Invention 260: claim 63 completely,  
and claims 1-20, 57-59 69-71, all partially

PR0172: nucleic acid with seq.ID.345, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.346 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.346 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for modulating the uptake of glucose or FFA by skeletal cells, method for stimulating the proliferation or differentiation of chondrocytes, and method for stimulating the proliferation of inner ear utricular supporting cells using the PR0172 protein.

Invention 261: claims 1-20, 57, 69-71,  
all partially

PR0265: nucleic acid with seq.ID.349, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.350 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.350 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR0265 protein.

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Invention 262: claims 1-20, 57, 69-71,  
all partially

PRO266: nucleic acid with seq.ID.353, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.354 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.354 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PRO266 protein.

Invention 263: claim 64 completely,  
and claims 1-20, 57, 60, 69-71, all partially

PRO344: nucleic acid with seq.ID.361, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.362 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.362 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, method for modulating the uptake of glucose or FFA by adipocytes, and method for stimulating the proliferation of T-lymphocytes using the PRO344 protein.

Invention 264: claims 1-20, 59, 69-71,  
all partially

PRO301: nucleic acid with seq.ID.365, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.366 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.366 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the proliferation

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or differentiation of chondrocytes using the PR0301 protein.

Invention 265: claims 1-20, 57, 69-71,  
all partially

PR0337: nucleic acid with seq.ID.375, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.376 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.376 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR0337 protein.

Invention 266: claims 1-20, 65, 69-71,  
all partially

PR0526: nucleic acid with seq.ID.381, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.382 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.382 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of a cytokine from PBMC cells using the PR0526 protein.

Invention 267: claims 1-20, 57, 69-71,  
all partially

PR0322: nucleic acid with seq.ID.395, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.396 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.396 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR0322 protein.



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Invention 268: claims 1-20, 58, 69-71,  
all partially

PR0719: nucleic acid with seq.ID.399, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.400 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.400 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for modulating the uptake of glucose or FFA by skeletal cells using the PR0719 protein.

Invention 269: claims 1-20, 59, 69-71,  
all partially

PR01312: nucleic acid with seq.ID.481, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.482 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.482 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the proliferation or differentiation of chondrocytes using the PR01312 protein.

. Invention 270: claims 1-20, 57, 69-71,  
all partially

PR01286: nucleic acid with seq.ID.499, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.501 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.501 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR01286 protein.

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Invention 271: claims 1-20, 57, 69-71,  
all partially

PR01279: nucleic acid with seq.ID.505, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.506 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.506 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood using the PR01279 protein.

Invention 272: claims 1-20, 57, 60, 69-71,  
all partially

PR01338: nucleic acid with seq.ID.511, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.512 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.512 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of TNF-alpha from human blood, and method for modulating the uptake of glucose or FFA by adipocytes using the PR01338 protein.

Invention 273: claims 1-20, 57, 65, 69-71,  
all partially

PR01343: nucleic acid with seq.ID.513, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.514 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.514 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the release of

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TNF-alpha from human blood, and method for stimulating the release of a cytokine from PBMC cells using the PR01343 protein.

Invention 274: claims 1-20, 59, 69-71,  
all partially

PR01868: nucleic acid with seq.ID.537, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.538 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.538 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also method for stimulating the proliferation or differentiation of chondrocytes using the PR01868 protein.

Invention 275: claims 25-28, 32-34, 37,  
38 completely, and claims 1-20, 69-71,  
all partially

PR01801: nucleic acid with seq.ID.545, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.546 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.546 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR01114 and/or PR04978 using its interaction with PR01801, method for linking a bioactive molecule to a cell expressing PR04978 and/or PR01114 through the use of PR01801, and method of modulating at least one activity of said cell thereby.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

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PCT/US 00/32678

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